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Example 1; Page 45-46; 52pp; English

WPI; 2000-602195/57. Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 Synechocystis species) and phycoerythrobilin conjugate, fluorescent markers for biological research -	arias JC;	(REGC) UNIV CALIFORNIA.	19-MAR-1999; 99US-0272809.	14-MAR-2000; 2000WO-US06607.	28-SEP-2000.	WO200056355-A1.	Synechocystis sp.	Phytochrome; fluorescent apophytochrome; bilin; Cph.	Synechocystis sp phytochrome-related gene Cph2.	01-FEB-2001 (first entry)	AAB26593;	SULT 1 B25593 AAB26593 standard; protein; 1276 AA.	ALIGNMENTS		216 3.3 1129 19	223.5 3.4 199 15 218.5 3.3 1128 22	224 3.4 296 21	229 3.5 1404 22 228 3.4 738 22	229 3.5 851 22	229 3.5 746 22 229 3.5 746 22	230.5 3.5 426 22	246 3.7 528 22 246 3.7 1142 19	25/.5 3.9 /48 21 250 3.8 1025 22	265 4.0 371 21	273 4.1 509 22 267 4.0 745 22	280 4.2 895 22	287 4.3 750 21	291 4.4 339 22 288 4.4 1371 21	295 4.5 532 14	297.5 4.5 498 20	299 4.5 387 22	299.5 4.5 499 21	332.5 5.0 950 21	349 5.3 481 21	351.5 5.3 1014 22	375 5.7 844 2	
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The present invention is related to fluorescent apophytochrome-bilin conjugates, known as phytofluors. An apoprotein known as Cph2 from Synechocystis species is used as the apophytochrome and the bilin is preferably phycocrythrobilin. The phytofluors are useful as fluorescent markers for biological research. The phytofluors have a long wavelength absorption maxima, a high molar absorption coefficient and the

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ylate cyclase; cellulose production; cdg2 op
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388
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275
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271
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Pred. No. 3.1e-78;
0; Mismatches 0;
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Query Match 10.4
Best Local Similarity 26.2
Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide sequence from Acetobacter cdg operon - cyclic di:guanosine mono:phosphate degradation enzymes 3-phosphodiesterase isozyme
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DB; AAQ43661.
VEALVRWOHPRLGQVAPDVFIPLAEELGLINHLGOWVLETACATHOHFFRETGRRLRMAV
                                                               \verb|atrqakedgrglfrfagqeknqvaqdrlvlgsalrdslskgmlnlnyqpqvetmtgglyg|
                                                                                           ALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTGKLLG
                                                                                                                                                  vvpecs-heraekfaenlinaiarplqvgentlsisccvgistfpangpdsesllshada
                                                                                                                                                                      AQVASTQL---YMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALY---EG
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Pred. No. 4.4e-50;
}1; Mismatches 322;
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RESULT
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                         Query Match
Best Local Similarity
Matches 208; Conserv
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                                                                                                                                                                                                   phosphodiester bond
See also AAR38156.
                                                                                                                                                                                                                                                    phosphodiesterase A,
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Tal R, Wong |
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                                                                                                                                                                                                                        amino acid sequence of protein PDEA3 was deduced from the 1st. reading frame of the cdg3 operon. The protein is a digranylate sphodiesterase A, i.e. it enzymatically cleaves a single sphodiester bond in c-di-GMP to yield the linear dimer pGpG.
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DB; AAQ43662.
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92; Mismatches 199;
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Matches 13(
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N-PSDB; AAQ14257.
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77; Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter; plasmid; insecticidal protein; Bacillus thuringiensis; Bacillus sphaericus; larva; mosquitoe; Culex; Anopheles; Psorophoa; Mansonia; Aedes.
                                                                                                                                                                                                                                                                                                                                              Caulobacter transformed with a plasmid contg. a gene encoding insecticidal protein derived from Bacillus thuringiensis or Bacillus sphaericus will proliferate in ag. environment. They may be consumed by larvae of mosquitoes and are lethal to
                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 16-21; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                       Expression of insecticidal protein - by transforming Caulobacter with plasmid contg. gene coding for insecticidal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SILM-) SILMARAN SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C6-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus sphaericus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR41019 standard; Protein;
                                                                                                                               126
                                                                                                                                                                                                                            536 ERLLS----TEQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKN 591
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                                                                                                                                                                                 TYOFYRPODSAPMLDRUTLESDLROALTNOEFVLYFOPQVALDTGKLLGVEALVRWQHPR 651
                                                                                                WLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSS
                                                                                                                                                                      nhrffdekmnelvikkdqiermirlalernefsvhyqlqieattgkirgfealvrwkspe
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1993-298916/38.
DB; AAQ48715.
kewncdfvqgyyfsrpvssdilvecl
                                                    LGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRLRMAVNISARQFQDEK 711
                                                                                                                                                                                                                  ekmlsslrdsfvqpftihgqitfvqmslgiasypidgvtqeellkhadiamykakelggn
           QKMGCHLGQGYFLTRPLPAEAMMTYL 857
                                         130;
                                                                                                                                                                                                                                                                                                                                     Anopheles,
                                                                                                                                                                                                                                                                                                                 340
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
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                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91JP-0160963
                                                                                                                                                                                                                                                                                                                                     Psorophoa, Mansonia
                                                                                                                                                                                                                                                                      9.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TANABAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain SSII-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene ORF-1 prod
                                                                                                                                                                                                                                                         77; Mismatches 115;
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                                                                                                                                                                                                                                                                     Score 635; DB 14;
Pred. No. 5.2e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                      and Aedes
                                                                                                                                                                                                                                                                                 Length 340;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A 4.1 bp Sau3AI-PstI sequence (given in AAQ87268) of B. sphaericus SSII-1 included 2 ORFs, the first encoding the protein given in AAR75409, and the second encoding mtx mosquitocidal toxin (AAR75410).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterium expressing Bacillus sphaericus mosquitocidal toxin - b lacking protease(s) that degrade the toxin, for control of Culex, Aedes and Anopheles mosquitos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-215263/28.
N-PSDB; AAQ87268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus sphaericus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR75409 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27-28; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porter AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mosquito; Culex; Aedes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B. sphaericus mtx toxin-associated
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                                                    832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 ERLLS----TPQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKN 591
     306
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                                                                                                                                                                                               LGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRLRMAVNISARQFQDEK
                                                                                                                                                                                                                                                                                                                                                                                                             nhrffdekmnelvikkdqiermirlalernefsvhyqlqieattgkirgfealvrwkspe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKMGCHLGQGYFLTRPLPAEAMMTYL 857
                                                                                                 kewncdfvqgyyfsrpvssdilvecl
                                                                                                                                                                                                                                                                                                         {\tt lglvspedfipiaektglitqidewvmyqaclknvelqhqfgypflmsvnisalqlgrad}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      control agent; mosquitocidal toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SINGAPORE NAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB02628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 635; DB 16;
; Pred. No. 5.2e-46;
77; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 340;
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                                                                                                                                                                                                                                                                                               complementary to (I) that are specific for particular species of microorganisms can be used to identify particular microorganism species in clinical specimens, therefore, providing a rapid and dependable method by which to identify the causative agents of a bacterial infection. Also, antibodies generated against proteins translated from mRNA transcribed from proliferation required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner. AAH84371 and AAH84670 represent sequencing primers used in the isolation of E. coli growth and proliferation related sequence, which are used in an example from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic for screening
                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli;
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                                                                                                                                   401
                                    262
                                                                   459
   518
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                                                                                                                                  RSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALY--
FTILLTQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKF
                               adnnkvgvvyldldnfkkvndayghlfgdqllrdvslai---lscl-ehdqvlarpggde
                                                                -EGKMVGVLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDG
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                                                                                                                                                                                                                                                      661 AA;
                                                                                                                                                                 9.2%; Score 607; DB 22; ilarity 31.6%; Pred. No. 4.5e-43; Conservative 110; Mismatches 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US30950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids that inhibit Escherichia coli proliferation, useful for homologous genes and for designing expression vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth; proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microorganism.
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                                                                                                                                                                    165;
                                                                                                                                                                                                Length
                                                                                                                                                                  Indels
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Query Match
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Matches 134; Conser
                                                                                  The amino acid sequence of protein DGC2 was deduced from the 2nd. open reading frame of the cdg2 operon. The protein has diguanylate cyclase activity, i.e. it enzymatically converts two molecules of GTP to bis-(3.5')-cyclic diguanylic acid.
                                                                                                                                        Claim 5; Page 80-83; 98pp; English
                                                                                                                                                             Polynucleotide sequence from Acetobacter cdg operon cyclic di:guanosine mono:phosphate degradation enzym 3-phosphodiesterase isozyme
                                                                                                                                                                                                                                                                                                                                                                                                 Cyclic diguanylate; diguanylate phosphodiesterase; diguanylate cyclase; cellulose production; cdg2 operon.
                                                    Sequence
                                                                                                                                                                                                         N-PSDB; AAQ43661.
                                                                                                                                                                                                                                       Ben-Bassat A, E
Tal R, Wong HC;
                                                                                                                                                                                                                                                                                                                                       10-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                               Acetobacter xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR38154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR38154 standard;
                                                                                                                                                                                                                   WPI; 1993-197062/24.
                                                                                                                                                                                                                                                                                            29-NOV-1991;
                                                                                                                                                                                                                                                                                                                 14-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                           W09311244-A
                                                                                                                                                                                                                                                                                                                                                                                                                                   Acetobacter diguanylate cyclase
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25.3%;
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Score 447.5;
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Conservative

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Indels

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Gaps

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                                           Ben-Bassat A,
Tal R, Wong
                                                                                                                                                           29-NOV-1991;
                                                                                                                                                                                                         14-OCT-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acetobacter xylinum.
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                                                                                                              (WEYE ) WEYERHAEUSER CO
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                                                                Benziman M,
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PN XXX XXX AXX

AAB26597 st. AAB26597; 01-FEB-2001

(first

entry)

Synechocystis sp phytochrome-related

gene Cph6. ome; bilin;

fluorescent apophytochrome;

Phytochrome; fluo Synechocystis sp RESULT 12 AAB26597

standard; protein;

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Best Local Similarity
Matches 133; Conserv
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See also AAR38149-R38150 and AAR38152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequence from Acetobacter cdg operon - ecyclic diguanosine mono:phosphate degradation enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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530 vetkgqmevlremgadriqgfyisppisa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88
                IESEAQLQRLQKMGCHLGQGYFLTRPLPA 850
                                                                                                                                                                     lddfglatlpisvlrtisftqakisrklvkdietspqargvvahliglahafglsvtvsg
                                                                                     IDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEG
                                                                                                               srldllnigfqndleaeikrqggkaadyvleisesvlagrrsdrvlqrlqelselgfqlt
                                                                                                                                           SARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVV-LLHRLREEGVQVA
                                                                                                                                                                                                  RLGQVAP----DVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRL----RMAVNI 702
                                                                                                                                                                                                                                hqarmfdmtlhqhaleraqilndaregvmkdqfelyyqpimnfstgkcdqieallpwhhp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 77-79; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA;
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Pred. No. 1.4e-27;
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Matches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived Synechocystis species) and phycoerythrobilin conjugate, useful a fluorescent markers for biological research -
                                                                                                        1016
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                                                            VAIAIHQGELYEQLETANIRLQQISSLDAL-TQVGNRYLFDSTLEREWQRLQRIREPLAL
                                                                              qshlrqchidflarlqvranlvlplindailwgllcihqcdssrvweqteidllkqitnq\\
                                                                                                                          rvvifqfspdsdfsvgnivaesvlapfkpiinsaieetcfsnnyaqryqqgriqviedih
                                                                                                                                                RVVLFKF--NSQWS-GQVVTESHNDFCRSIINDEIDDPCFKGHYLRLYREGRVRAVSDIE 1015
                                                                                                                                                                                                                                        QGNVGDRPLPNSLNRENPWTEKLHDYVLLKE------
                                                                                                                                                                                                                                                                                EAQLQRLQKMGCHLGQGYFLTRPLPAEAMMTYLYYPQILDFGPTPPLPKVALPETETEAG
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                                                                                                                                                                                                                                                                                                                           SLSILKQLPIHRLKIDKS-----FVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIES 824
                                                                                                                                                                                                                                                                                                                                               tklipeelile--edliaecirqgqrintyetqrqrkdgtkidvaltispirdehknvvg 302
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                                                                                                                                                                                                                -----diptlyenknfwqksqegqvltteyrmrhkngswrwlrsrevvfarddygqvt
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119; Conserv
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                                                                                                                                                                                           ----RLQQRNVKEKLVLKIANKIRASLNINDILYSTVTEVRQFLNTD
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Pred. No. 8.4e-23;
0; Mismatches 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived from Synechocystis species) and phycoerythrobilin conjugate, useful as fluorescent markers for biological research -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 48; 52pp; English.
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-ILSETSLEGAINVTEALQ-VEVANLAIPHTVSGTGHVTLSIGIAVYTPERHINPNALVK
                                                                                                                                                                                                                                   ATQVAIAIHQGELYEQLETANIRLQQI-----SSLDALTQVGNRYLFDSTLEREWQRLQ 1126
                                                                                                                                                                                                                                                                                                                    DIEKADLADCHKELLRHYQVKANLVVPVVFNENLMGLLIAHECKTPRYWQEEDLQLLMEL 1072
                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFLNTDRVVLFKFNSQWSGQVVTESHNDFCRSIINDEIDDPCFKGHYLRLYREGRVRAVS 1012
                                                                             hvte---
                                                                                                                               RIREPLALLLCDVDFFKGFNDNYGHPAGDRCLKKIADAMAKVAKRPTDLVARYGGEEFAI 1186
                                                                                                                                                                                 tvqvglalersdllaqqkiaeveqrqmrekmqkralellmevdpvsrgdltir----a
                                                                                                                                                                                                                                                                                        diynagltpchigqlkpfevkanlvapinykgnllglliahqcsgprdwhqneidlfgql
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27.5%;
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Pred. No. 5.5e-21
72; Mismatches 15
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RESULT AAG90902 ID AAG90902 ID AAG90902 ID AAG90902 ID AAG90902 ID AAG9002 ID
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                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nakagawa
Tateishi
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07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; organic acid synthesi:
                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                      GQAVEAD----GAVLYIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRG--QPSAAM 283
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DB; AAH66121.
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157; Conserv
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Senoh A,
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2000JP-0159162.
2000JP-0280988.
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                                                                                                                                                           107;
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tern of a gene and identifying homologous
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                                                                                                                                                                                                                                                                                                                                               RESULT 15
Fluorescent apophytochrome-bilin
                         WPI; 2000-602195/57.
                                                                                                                                                                                                                                                Synechocystis sp phytochrome-related
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                                                                                                                         14-MAR-2000;
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                                                                                                                                                                         WO200056355-A1
                                                                                                                                                                                                Synechocystis
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Query Match 5.3%; Score 349; DB 21; Length 481; Best Local Similarity 32.8%; Pred. No. 5.6e-21; Matches 80; Conservative 51; Mismatches 83; Indels 3
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244 slrm 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related protein from Synechocystis sp.
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7, 2002, 18:55:13
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Result
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Sequence 2, Appli	Sequence 2, Appli	Sequence 170, App	Sequence 2, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 8, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 1, Appli	2	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 33, Appl

ALIGNMENTS

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APPLICATION NUMBER: US 07/800.
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BOTTNEY, SCOTT R.
REGISTRATION NUMBER: 34.298
REFERENCE/DOCKET NUMBER: 8145-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELERX: 66141 PENNIE
TELERX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5/3302
Patent No. 5/3202
Patent No. 5/
TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Acetobater:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: (FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Ben-Bassat, Arie
APPLICANT: Ben-Bassat, Brie
APPLICANT: Wong, Hing C.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
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Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
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RESULT 2
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Sequence 8, Application PC/TUS9208756A
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Best Local Similarity
Matches 228; Conserv
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGAVGRADVLEFTVDQPKI------SADVLLSAMEQAIDPMVVIDEHNLI 54
                                                                                                                      GVETEQQWRLLEELHCDVMQGYLFSKPLP
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                                                                                                                                                                                                                                                                                                                                VEALSRWHHPTLGNIYPSRFIAVAEETGQIEAIGRWSLEEACSQMVKWDRDGVRVPTVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -RVVSTSMPFCALAIEQSETRQHIAQLSNFDSLTGL----LNRTSLHNIIERLIMRGGD
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18; Pred. No. 9e-55;
130; Mismatches 323;
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                  Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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FILING DATE: 19921014
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Acet
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APPLICANT:
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REGISTRATION NUMBER: 34,298
REGISTRATION NUMBER: WEYR 20050
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                                                                                                                                                                                                                                                            71 LGLHFPVEDIPPQAREELGNQRKMIAVDVAHRRKKSHELS------GRISPT-----E
                                                VGQAVEADGAVLYIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRGQPSAAMEPMAA 288
                                                                                     VLQNDVLQALASDMSI - -
                                                                                                         EQEWETMALLSKEVSLAITQSQLSRQVHQQQVQEALVQRLETTVAQYGDRPETWQYALET 228
                                                                                                                                                        RANGEYVCGELSISRVQVNDCGKIYYIA-----VMKD-----VTEQSRQRKIL 157
                                                                                                                                                                                      HSNGHY-----TTVDSCHIQYLLAMGVLSSLTVPVMQDQQLWGIMAVHHSKPRRFT 168
                                                                                                                                                                                                                            IFFNAAAEKIWGCSREEVMGRNVSCLVPEPERDRHDDYINRNRETGVGRIVGTSREVEFR 114
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Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
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VENTION: CYCLIC DIGUANYLATE
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RESULT · 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC ENZYMES
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                                                                          FILING DATE
                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                      STREET: 2730 San
CITY: Menlo Park
STATE: Californi
FILING
                                                                                         APPLICATION NUMBER:
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 DATE:
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Ben-Bassat, Arie
Calhoon, Roger D.
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 29-NOV-1991
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                 US 07/800,218
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TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
FENGTH: 740 amino acids
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Best Local
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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FRETGRRLRMAVNISARQFQDEKWLNSVLECLKTTGMPPEDLELEITESLMMEDIKGTVV 748
                                                                                                                                                                                                                                PDSESLLSTADVALRQAKEDGRGVFRFANLEKNQVAQDRLVLGSALRDSLAKGMLNLHYQ 485
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                                      LLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVID 808
                                                                                                                                                                                            PQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHF 688
                                                                                                                                                                                                                                                                                                          VLSRSGGDEFVVVVPD-CPHKEATDFAEHLLASMTMPMQIGQNTLTISCSIGISTYPDNG
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                                                                            DRDGIHVPTVAVNLSAVHFRNRALPEHIAALLKDHNLKPSRLTVEITESVMMDNSRDTEE
                                                                                                                                                        PQVRTHTLELSGVEALSRWHHPHLGNIFPSRFIAVAEETGQIEAIGRWSLLEACRQIVKW
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                                                                                                                                                      Query Match
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TELEX: 278356
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Acet
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APPLICATION NUMBER: US 07
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 415-433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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 IM--AVHHSKPRRFTEQEWETMALLSKEVSLAITQSQLSRQVHQQQVQEALVQRLETTVA 213 : | : | : | : | : | : | : | : | : |
                                                   PTLHQAGHDAFVERSRGSSHNRIVGTSREVEFTRSDGEYICGELSLSKVVNDDKRIFFMG 118
                                                                                   PTEHSNGHYTTVD-----
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Gelfand, David H.
Ben-Bassat, Arie
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
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                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08309512 Patent No. 5759828
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APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                  APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC
NUMBER OF SEQUENCES: 63
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                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 LMRGQPSAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VMKNVTNESQQRK----
                                                   COUNTRY:
                                                                      STATE:
                                                                                                   STREET:
                                                                                    CITY: Menlo Park
                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                AAPAAK 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPPLPK 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVID 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRETGRRLRMAVNISARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVV 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LANGLNLETVAEGIESEAQLQRLQKMGCHLGQGYFLTRPLPAEAMMTYLYYPQ-ILDFGP 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLQSIRNIGCGLSMDDFGTGYSSLSRLTRLPLTEIKIDRSFINDFEHDTNAQAVTMAVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRDGIHVPTVAVNLSAVHFRNRALPEHIAALLKDHNLKPSRLTVEITESVMMDNSRDTEE 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHF 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDSESLLSTADVALROAKEDGRGVFRFANLEKNQVAQDRLVLGSALRDSLAKGMLNLHYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQ 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FAIFMLD-----IDRFRDINDALGHVYADQFLIEIAARIRS----IAKEDY 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PGT-----VAVLMLITPDGQLRVLS---SPTLPKRYRASLE----SLYVSSSELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYGDRPETWQYALETVGQAVEADGAVLYIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGSRLGMTVVTEGVETEQQRDLLEKLNCDVMQGYLFAKPLAPDDFEKWMRHHQTIRQMLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQVRTHTLELSGVEALSRWHHPHLGNIFPSRFIAVAEETGQIEAIGRWSLLEACRQIVKW 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSRWHGDGFTILLTQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLVPTWNRSERKLAQVASTQ-----LYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQ 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LQQCFCTPVSTRSGQVKGIFALYSREDQGRNTQPQRIVDSCIPFCALAFEQ-----
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                                   94025
                                                                     California
                                                                                                                                                                                                    Benziman, Moshe
Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
                                                                                               E: Pennie & Edmonds
2730 Sand Hill Road
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                                                   U.S.A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 765 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
ORGANISM: Acetobater xylinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: |
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 81
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US (
FILING DATE: 29-NOV-199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
SOFTWARE: Pataning
                                                                                                                                                                         774 ILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQK 833
                                                                                                                                                                                                                            574 EHIAALIKDHNLKPSRLTVEITESVAMDNSRDTEEVLQSIRNIGCGLSMDDFGTGYSSLS
                                                                                                                                                                                                                                                                                                        514 NIFPSRFIAVAEETGQIEAIGRWSLLEACRQIVKWDRDGIHVPTVAVNLSAVHFRNRALP 573
                                                                                                                                                                                                                                                                                                                                                                                   454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 RDINDALGHVYADQFLVEIAGRIRS----IAKDDYVLSRSGGDEFVVVVPD-CEGKQIEE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 KRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDGFTILLTQISDNQEMIP 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 MAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALYE--GKMVGVLVIAMDRF 473
                                                                         694 LNCDVMQGLYFAKPLA---
                                                                                                           834 MGCHLGQGYFLTRPLPAEAMMTYLYYPQILDF----GPTPPLPKVALPETETEAGQGNVG 889
                                                                                                                                                                                                                                                                  714 NSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLS 773
                                                                                                                                                                                                                                                                                                                                            654 QVAPDVFIPLAEELGLINHLGOWVLETACATHQHFFRETGRRLRMAVNISARQFQDEKWL 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 IAHKLLETIGRPLQIGQNTLSISCSIGISTFPANGPDSESLLSHADTAMRQAKEDGRGIF 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534 LCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKNTY 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 LALEQHATKTHLTQLARYDSLTGLLNRGALHR----VMEDIIAQPGNRTLAIFMLDIDRF 338
738 GKP 740
                                     890 DRP 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                     QFYRPQDSAPMLDRLTLESDLRQALINQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLG 653
                                                                                                                                                   RLTRLPLTEIKIDRSFINDFEYDTNAQAVTMAVIGIGSRLGMTVVTEGVETEQQRDLLEK
                                                                                                                                                                                                                                                                                                                                                                                 RFANLEKNQVAQDRLVLGSALRDSLAQGMLQLHYQPQVRTHTLELSGVEALSRWHHPHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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EM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 651.5; DB 1;
Pred. No. 4.5e-52;
)2; Mismatches 199;
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                                                                           --PQDLESWVRRGGAPAVIR---
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                                                                           --EIEAARAKKG
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                                                                                                                                                                                                                              633
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  Query Match 9.9%; Score 651.5; DB 5; Best Local Similarity 33.3%; Pred. No. 4.5e-52; Matches 161; Conservative 92; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: pr
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tal, No.... Moshe APPLICANT: Benziman, Moshe APPLICANT: Gelfand, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: WE TELECOMMUNICATION INFORMATION: TELEPHONE: 415-433-4150
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0: FILING DATE: 29-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                          594
                                                                                                                                                                                                                                                                             416 MAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALYE--GKMVGVLVIAMDRF 473
                                                                                 394
                                                                                                 534 LCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKNTY 593
                                                                                                                                                                                               474 KRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDGFTILLTQISDNQEMIP 533
                                                                                                                                                                                                                                      283 LALEQHATKTHLTQLARYDSLTGLLNRGALHR----VMEDITAQPGNRTLAIFMLDIDRF 338
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TELEX: 278356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 2001 Ferry I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bortner, Scott REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                        QFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLG 653
                                                                                                                                                             RDINDALGHVYADQFLVEIAGRIRS----IAKDDYVLSRSGGDEFVVVVPD-CEGKQIEE 393
RFANLEKNQVAQDRLVLGSALRDSLAQGMLQLHYQPQVRTHTLELSGVEALSRWHHPHLG
                                                                             TAHKLLETIGRPLQIGQNTLSISCSIGISTFPANGPDSESLLSHADTAMRQAKEDGRGIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetobater xylinum
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US-08-309-512-9
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US-08-309-512-9
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                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
           MOLECULE TYPE: p
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Acet
                                                                                                                                                                                                            NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: 81.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILING DATE: 29-NOV-1991
ATTORNEY/ACENT INFORMATION:
                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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TITLE OF IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 2730 Sand
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                              574 amino acids
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                                                                                                                                                                                                (415) 854-3694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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Calhoon, Roger D.
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Gelfand, David H.
               Acetobacter xylinum
                                                                NO
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                                                                                protein
                                                                                                                                                                                 PENNIE
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Best Local Similarity
Matches 136; Conserv
STREET: 2001...
CITY: San Francisco
STATE: CA
                                                                                                                                                            TITLE OF INVENTION: CYCLIC DIVERTILE OF INVENTION: METABOLIC
                                                                                                                                                                                                        APPLICANT: Ben-BappLICANT: Calhor APPLICANT: Wong,
                                                                                                                                                                                                                           APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Ben Bassat, Arie
APPLICANT: Calhoon, Roger D.
                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 MEVDQIEALLRWQHPERGLLAAEDFSDVFTDAGLAQAMGPRMIEAFRRDVC-----MWNE
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                                                              ADDRESSEE: Limbach and Limbach
STREET: 2001 Ferry Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VG-----VLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGD 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRLREE-----GVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGRRLR-MAVNISARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLL 750
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DIGUANYLATE

ON: CYCLIC DIGUANYLATE
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SOFTWARE: Patentin Releas SOFTWARE: Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/U FILING DATE: 19921014

PCT/US92/08756A

CLASSIFICATION:

APPLICATION DATA:

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY: UZIP: 94111

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0,

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                                                                                                  Sequence 6, Application US/08309512 Patent No. 5759828
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Best Local Similarity
Matches 136; Conserv
                                                            GENERAL INFORMATION: APPLICANT: Tal, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-433-8716
TELEX: 278356
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Ace
                     APPLICANT:
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      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bortner, Scott R. REGISTRATION NUMBER: 34,298
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                                                                                                                                                                                                                                                                                                                                            HRLREE------GVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGA 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KNADMAMYAAKRAGGKQSQMFTRNLRERAQARVSILSEARCGVERNQFEVYYQPIVNCNT 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDT 635
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                                                                                                                                                                                                                                                                                                                                                                                    KGQPPRQLAINLSRMDLIRDDYQRELEESLRRFNMSPDSFVLEVTEA-------ML 447
Tal, Ronny
Benziman, Moshe
Gelfand, David H.
Ben-Bassat, Arie
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US-08-309-512-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.4%;
Best Local Similarity 26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/1
APPLICATION NUMBER: US 07/1
FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: BOTTNEY, SCOTT R.
14,29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 854-369
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL:
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LENGTH: 580 amino acids
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APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE METABOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy
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REFERENCE/DOCKET NUMBER: 8145-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Menlo Park
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                       QRGLLAAESFRDVFLDAA---
                                                                                                                                                                                                                                      MIPLCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGK 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                             WRGNICNRAKDGTL--YWVATTIMPKHNSLG--AVEGYVATRFEITELMNTRDRLKSLAA 143
SARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVV-LLHRLREEGVQVA 761
                                                                                                                   HQARMFDMTLHQHALERAQILNDAREGVMKDQFELYYQPIMNFSTGKCDQIEALLPWHHP
                                                                           RLGQVAP----DVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRL----RMAVNI 702
                                                                                                                                                        NTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFYLYFQPQVALDTGKLLGVEALVRWQHP 650
                                                                                                                                                                                                LSLMLEKLLAELEAPIEVGNTMVNVSGSIGV-TPIASQESAESLQKNADIALYAAKRAGG 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 102; Mismatches 226; Indels
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415) 854-3694
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Pred. No. 6e-31;
                                     -LAQVMSPRLVKSFQNDMRMWNTSLDAYPNLTINL 409
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PCT-US92-08756A-6
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GENERAL INFORMATION:
                                                                                             Matches
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 580 amino acid
                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gelfand, David H.
APPLICANT: Ben-Bassat, Arie
APPLICANT: Calhoon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                            352 WVGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWEETQKLVPTWNRSERKLAQVAS 411
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  88
                                                                                          Local Similarity
nes 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bortner, Scott R. REGISTRATION NUMBER: 34,298 REFERENCE/DOCKET NUMBER: WE
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                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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TELEX: 278356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
WRGNICNRAKDGTL--YWVATTIMPKHNSLG--AVEGYVATRFEITELMNTRDRLKSLAA 143
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Gelfand, David H.
                                                                                          Conservative
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EM: PC-DOS/MS-DOS
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                                                                                          Score 425; DB Pred. No. 6e-3
                                                                           . 6e-31;
-= 226;
                                                                                                                                      Length 580;
                                                                                          Indels
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US-08-309-512-11
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ZIP: 94025

ZIP: 94025

COMPUTER READABLE FORM:

COMPUTER: TBM PC compatible

COMPUTER: TBM PC
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APPLICANT:
APPLICANT:
                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 29-NOV-1991
                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compa
OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel-
CURRENT APPLICATION DATA:
                                            REFERENCE/DOCKET NUMBER: 8145-008 TELECOMMUNICATION INFORMATION:
                                                                                                              FILING DATE: 29-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bortner, Scott R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                          NAME: Bortner, Scott R. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                        TELEPHONE:
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Gelfand, David H.
Ben-Bassat, Arie
Calhoon, Roger D.
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(415) 854-3660
15) 854-3694
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651 RLGQVAP----DVFTPLAEELGLINHLGQWVLETACATHQHFFRETGRRL----RMAVNI
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LDDFGLATLPISVLRTISFTQAKISRKLVKDIETSPQARGVVAHLIGLAHAFGLSVTVSG
                                                                   IDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEG
                                                                                                                                                                                                                                                                        QRGLLAAESFRDVFLDAA------LAQVMSPRLVKSFQNDMRMWNTSLDAYPNLTINL
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                                                                                                                                       SRLGLLNIGFQNDLEAEIKRQGGKAADYVLEISESVLAGRRSDRVLQRLQELSELGFQLT
                                                                                                                                                                                                    SARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVV-LLHRLREEGVQVA 761
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Hing C. NN: CYCLIC DIGUANYLATE METABOLIC ENZYMES Release #1.0, Version #1.25

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RESULT 12
PCT-US92-08756A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                    APPLICANT: Tal, Ronny
APPLICANT: Benziman, Moshe
APPLICANT: Gelfand, David H.
APPLICANT: Ben Bassat, Arie
APPLICANT: Ben Bassat, Arie
APPLICANT: Calhoon, Roger D.
APPLICANT: Wong, Hing C.
TITLE OF INVENTION: CYCLIC DIGUANYLATE
TITLE OF INVENTION: METABOLIC ENZYMES
NUMBER OF SEQUENCES: 11
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COUNTY 94111
ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
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ORGANISM: Acetobacter xylinum
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LENGTH: 493 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 SAENFQSF---LIVPLAADQQWYGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWE 390
                                                                                                                 ADDRESSEE: Limbach and Limbach STREET: 2001 Ferry Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
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                                                               COUNTRY:
                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMEDIKGTVVLLHRLR-----EEGVQVAIDDFGTGYSSLSILKQLPIHRLKI 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QSFHDDIQKWKEAGLPSLRLAVNLSHLDLLNLEQQIDLFSEIRELNLEPSTFILEVTEQI
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                                                                                                    San Francisco
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 127;
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INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: N
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,218
FILING DATE: 29-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 SAENFOSF---LIVPLAADQQWVGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWE 390
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TELEFAX: 415-433-8716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bortner, Scott R. REGISTRATION NUMBER: 34,298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release SOFTWARE: Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
----LQGRRAEKNRLRLRSLSGNGFGLAMDKFGYGTVRLSTLGELPFQSLKL 493
                                                                                                                                                                                                                                                         PYDG-ETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEF 623
                                                                                                                                                                                                                                                                                                                                       LLSRWHGDGFTILLTQISDNQEMIPLCERLLSTFQ----EPFFLQGQPIYLTASMGISTA 564
                                      MMEDIKGTVVLLHRLR-----EEGVQVAIDDFGTGYSSLSILKQLPIHRLKI 785
                                                                                                                  THQH-----FFRETG-RRLRMAVNISARQFQDEKWLNSVLECLKRTGMPPEDLELEITESL 738
                                                                                                                                                       EVYYQPILNARTGRIEQAEALMRWHHPDRGLLSAGAFTDVFADSALAQ-----IMETHLV
                                                                                                                                                                                            VLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQWVLETACA 683
                                                                                                                                                                                                                                     PITGADTLEGLQKNADVAVYAAKQSGGKQARMFTPSLHKTTMERAKILTEARKGVELRQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETQKLVPTWNRSERKLAQVASTQLYMAITQQFVTRL-ITQQTAYDPLTQLPNWIIFNRQL 449
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                                                                           QSFHDDIQKWKEAGLPSLRLAVNLSHLDLLNLEQQIDLFSEIRELNLEPSTFILEVTEQI
                                                                                                                                                                                                                                                                                                               AISRLGGDEFAIILRR----SLKLMPL-ETILTKVQNLLEEPIMLDSATVRISGSIG--AT 270
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26.9%; Pred. No. 5.1e-23;
7ative 85; Mismatches 195;
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18;

US-09-090-793-11 ; Sequence 11, Application US/09090793 ; Patent No. 6140486

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Sequence 19, Applicat
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/090,793
CURRENT FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,650
EARLIER FILING DATE: 1997-06-04
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Calgene,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 499
TYPE: PRT
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                             ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TITLE OF INVENTION:
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   CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KATO, Seishi
APPLICANT: KONDO, Kiyosi
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APPLICATION DATA:
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                                                                                                                                                                                                                                                       USA
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Synthesizing Enzymes and Process for I
Eiscosapentaenoic Acid
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29.0%; Pred. No. 3.1e-19;
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                                         Version #1.30
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Best Local Similarity
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                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1105
                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
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REFERENCE/DOCKET NUMBER: 53
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 4
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                       458
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                             STREET:
STATE:
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                                                                                                                                                                                                                                                                                                                     VSLGVCTVVAVDDFEFKSESHIIGSQAALIADKALYHAKACGRNQ
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             Washington
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D.C.
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KONDO, Kiyosi
                                                                                                                                                                    YAZAWA, Kazunaga
YAMADA, Akiko
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Acid
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29.0%;
                                                                                                                         Gene Coding
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Pred. No. 5.2e-19;
                                Suite 500
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Process for Production of
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Eiscosapentaenoic
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,929
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/375,709
FILING DATE: 20-CAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,251
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: JP 4-147945
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
ABMENT AGENT METORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.5%; Score 297.5; DB 1; Length 525; Best Local Similarity 29.0%; Pred. No. 5.2e-19; Matches 100; Conservative 50; Mismatches 128; Indels 67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                1165 MAKVAKRPTDLVARYGGEEFAIILSETSLEGAINVTEALQVEVANLAIPHTVSGT-GHVT 1223
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458 VSLGVCTVVAVDDFEFKSESHIIGSQAALIADKALYHAKACGRNQ 502
                                                                                                  398 LSQQFYRAEDICARFGGEEFIMLFRDIPDEPLQRKLDAMLHSFAELNLPHPNSSTANYVT 457
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REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 53466/150/AAOK
                                                                                                                                                                                                                LTNIPNRRAFEQRLETYCQLLARQQIGFTLIIADVDHFKEYNDTLGHLAGDEALIKVAQT 397
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Search completed: June 7, 2002, 18:55:44 Job time: 183 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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               June 7, 2002, 18:53:06 ; Search time 37.51 Seconds (without alignments) 3268.728 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen
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ALIGNMENTS	A87341 G98327 AF2955 H98161 AH3125 E95895 H95270 C95367 AC2202 B75515 A69861 A69861 G97626 G97626 G97626 G97626
	sensory box/GGDEF hypothetical 91.8K GGDEF family prote hypothetical 91.8K GGDEF family prote hypothetical prote hypothetical prote probable kinase/es conserved hypothet hypothetical prote sensory box/GGDEF conserved hypothet sensory box/GGDEF probable phosphodi hypothetical prote GGDEF family prote hypothetical prote

Qy 301 SVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAENFQSFLIVPLAADQQWVGSLILLR 360 	Qy 241 YIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRGQPSAAMEPMAAVQSTWEKPRPFT 300	Qy 181 EVSLAITQSQLSRQVHQQQVQEALVQRLETTVAQYGDRPETWQYALETVGQAVEADGAVL 240 	Qy 121 GHYTTVDSCHIQYLLAMGVLSSLTVPVMQDQQLWGIMAVHHSKPRRFTEQEWETMALLSK 180	Qy 61 AVNRAALPSLIGLHFPVEDIPPQAREELGNORKMIAVDVAHRRKKSHELSGRISPTEHSN 120 	Qy 1 MNPNRSLEDFLRNVINKFHRALTLRETLQVIVEEARIFLGVDRVKIYKFASDGSGEVLAE 60 	Query Match 100.0%; Score 6614; DB 2; Length 1276; Best Local Similarity 100.0%; Pred. No. 0; Matches 1276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	probable phytochrome s110821 - Synechocystis sp. (strain PCC 6803) C:Species: Synechocystis sp. A; Variety: PCC 6803 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999 C;Accession: S75801 R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys A;Reference number: S74322; MUID:97061201 A;Resesiton: S75801 A;Accession: S75801 A;Accession: S75801 A;Residues: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1276 <kan> A;Cross-references: EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BAA10536.1; PID:d101 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Superfamily: phytochrome homology C;Keywords: Chromoprotein; phytochromobilin F;1-416,Domain: phytochrome homology #status atypical <phyt> F;129/Binding site: phytochromobilin (Cys) (covalent) #status predicted</phyt></kan>	RESULT 1 S75801

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RESULT 2
AD1953
hypothetical protein all1175 [imported] -
C;Species: Anabaena sp.
A;Note: Anabaena sp. (strain PCC 7120) is
C;Date: 14-Dec-2001 #sequence_revision 14-
C;Accession: AD1953
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A; Status: Process A; Status: Type: DNA
A; Molecule type: DNA
A; Residues: 1-880 < KUR>
A; Cross-references: GB: BA000019; PA; Cross-references: GB: BA000019; PA; Cross-references: Strain PCC
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD1953
A;Status: preliminary
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LKSINCQDVQGFLFHKPLSAE
                        LOKMGCHLGOGYFLTRPLPAE
                                                   SLSRLQLLPLHNLKIDGSFIKALTTDSKVAHIVKAIVTLGRSLGLRLTAEGVEKQEELDF
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C 7120
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Pred. No. 8.5e-54;
8; Mismatches 232;
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RESULT C83070 conserved hypothetical protein PA4601 [imported] C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change Pseudomonas aeruginosa (strain

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A; Nolecule type: DNA
A; Residues: 1-1415 <STO>
A; Cross-references: GB: AE004874; G
A; Cross-references: GB: AE004874; G
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, LOTY, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                              QIARAIIAMAHSLNLMVIAEGVESQAQLDFLREHGCDEVQGYLFGRPMPAE-QFGMLYAS
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Pred. No. 1.6e-50;
2; Mismatches 263
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A; Gene: CC3094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensory box/GGDEF family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: D87632
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A; Residues: 1-748 <STO>
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                                                                                                           MGCHLGQGYFLTRPLPAEAMMTYLYY------PQILD-FGPTPPLPKVALPETET---
SPVAERTGEGSRG
                                                                                                                                                LCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKNTY
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                                                                                                                                                                                      ILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQK 833
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                                                                                                                                                                                                                                                  NSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLS
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                                 ----EAGQGNVG
                                                                         QGCAEIQGYFISRPAPASEIAKMLGVEGRADLGAPSVLSPIGANPPPPQ-AGQEVRTAPS
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Pred. No. 2e-48;
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L.; Venter, J.C.; Fraser,
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aft, D.H.; Ko
C.: Fraser, C
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hypothetical protein slr(C;Species: Synechocystis A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequ

#sequence_revision

25-Apr-1997

#text_change 08-Oct-1999

protein slr0359

Synechocystis

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RESULT S76102

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A;Molecule type: DNA
A;Residues; 1-1244 <KANN
A;Cross-references: EMBL:D63999; GB:AB001339;
A;Note: the nucleotide sequence was submitted
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; 1
DNA Res. 3, 109-136, 1996
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                                                                                                                                                                                                                     NTIKVDRSFVNTMEPNNQNTAIVHTIVTLAHTLGLDVIAEGIETERHLTQLHWLGCDAGQ
                                                              HRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQKMGCHLGQ
                                                                                                    SSTNLAPQDLKLEITESLLIDNLNLAADVLKSLRQRNIQISLDDFGTGYSSLSYLHRFPI
                                                                                                                     KRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPI 780
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                                                                                                                                                              EETGLIVPMGDWILWEASRQILELKQSFPQLS--HLQVSINVSSRQLRDQRLLKTVDEIL
                                                                                                                                                                                  EELGLINHLGQWVLETA----CATHQHFFRETGRRLRMAVNISARQFQDEKWLNSVLECL
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Pred. No. 5.9e-47;
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Watanabe, A.; )
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Nature 406, 959-964, 2000
A; Title: Complete genome sequ
A; Reference number: A82950; M
A; Accession: H83574
A; Actatus: preliminary
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                                                                                              KLSPLAAYSPLLSRWHGDGFTILLTQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTAS
               MGISTAPYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQAL 618:||: | ||: ||:||:||:||
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VGIALFPKDGDDAPTLVKNADAAMYRAKSRGRSRIEYYTRELTYLATERMALETELRRAL
                                                                        QLRDV----DTVARLGGDEFIILLPGLHQESDAEHVARKLLNAFTAPFQADGHEFFVSAS
                                                                                                                                                 LPNRLLFESRLNHALDEAREESRPGAVLFIDLDRFKHINDSLGHPIGDLLLKAIAERLRD
                                                                                                                                                                   LPNWIIFNRQLTLALLDALYEGKMYGYLYIAMDRFKRINESFGHKTGDGLLQEVADRLNQ 498
                                                                                                                                                                                                                                                                 LSFEAWEETQKLVPTW-----NRSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQ 438
                                                                                                                                                                                                                                                                                                         RSPSILSSGQHDSSFYLAMWNQLERDGHWQGEIWNRRKTGELYPEW----
                                                                                                                                                                                                                                                                                                                                    IAPPESLSAENFQSFLIV---PLAADQQWVGSLILLRKEKSLVKHWAGKRGIDRRNILPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
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K.; L
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hypothetical protein all4225 [imported] - Anabaena sp. (strain PCC 7120) (Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120) is a synonym of Nostoc sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002 C;Accession: AB2334 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, 1 DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                            Qy
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MEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGAD
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                                                                          NQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQWVLE
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                                                                                                                             RNEIVVYYQPIIDLQTKQITAVEALVRWQHPTRGLVSPAKFIPIAEANGLIVEIGEWVLR
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                                                      TACLQNRTWQLAGLPPIRMSVNLSARQFEESNLVELVSEIIQESGLHPSYLELEVTESSL
                                                                                                                                                                                              TTINQPDNLHDVDQLLQQAHVALYQAKQQGRSQHQFYSPEINAQLQERLALENELHGALE
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Similarity

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C; Accession: E83610
R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoquchi, S.D.; Warre adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                C; Genetics:
A; Gene: PA0
                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein PA0285 [imported] -
C; Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                             A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337 A;Accession: E83610
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                                                                                                                                  A;Cross-references: GB:AE004466; GB:AE004091; A;Experimental source: strain PAO1
                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-760 <STO>
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12.6%; Score 830.5; DB 2; ilarity 33.3%; Pred. No. 4.2e-45; Conservative 104; Mismatches 248;
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K.R.; Kas, A.;
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Qy δÃ Š Вþ δÃ 밁 Q δÃ δÃ δÃ Š 멍 뫄 B 밁 뫄 망 В Š B 599 326 270 345 174 420 214 QYGDRPETWQYAL--ETVGQAVEADGAVLYIAPDLTGSVAQHYQWNLRFDWGN--WLETS Local Sin hes 238; VRWQHPRLGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRLR-MAVNIS VLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDGFTILLTQ SRIFNRGGLEERIANALEESGLEPRYLELEVTESAVMEDFEQSLULLCRLRILGVULAID VRWQHPERGLVPPGEFVPVAEECGLIAALDNWVLKRACRQMRE-WQQRGVELEFVAVNVS -----RGR-----VLRDALGKPLHYTGVA-----RDITLQRLKEDHLRQAA LWQELMRGQPSAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQ-----ELGDPIETWKKRLHPEEYATVLEAHRNHL---QGLTDNLDHIYR--LRHKDGDYRWIHS-ARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAID AKDSGRNAYAFYTRVLTARARAHVQVESALRHALEHDELRVHYQPVHDLASGRIVGVESL AKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTGKLLGVEAL NDDPEAVARLSQRILDGFNAPFDIHCQPIYISASLGVSLYPEDASDVDHLMQHADAALFQ ISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETÄESLLKFAEIALTR LLLIDLDHFKHINDSLGHTTGDMLLKEVSKRLQHQLDERC----LLSRLGGDEFAILV-E ELDFLAH-KLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALYEGKMVG ALREQDVWSGEIWNRRKSGEIYPQWLHIRAV--RNDQGQLTHYVGVFSD--LSSIKRSEN PLAADQQWVGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWEETQKLVPTWNRSER AVFDSTREGYLYTDAQAVIYHVNPSFERITGYRSEDYLGKTPAILRSGRQDQAFYQRLWL HDSLTGLPNRVLLRERIEQALENGKDRTVAGA Indels 125; Gaps 763 644 479 419 364 464 404 703 539 584 524 325 269 344 173 658 598 322 18;

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A, Reference number: S74322; MUID:97061201
A; Accession: S75626
A; Status: nucleic acid sequence not shown; trans
A; Molecule type: DNA
A; Residues: 1-696 < KRAN>
A; Cross-references: EMBL:D90912; GB:AB001339; NI
A; Note: the nucleotide sequence was submitted to
C; Superfamily: hypothetical protein s111895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YPO0998 [imported] - Yersinia pestis (strain
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-
                                                 RESULT
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                                                                                                                                                                                                                            FQAPDLLPTILRILAESSLPPHRLEVEITENIVMQNVTATQNLLNALQSHGIRLSMDDFG
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Pred. No. 1.4e-44;
9; Mismatches 184;
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Yamada, M.; Ya
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R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A. M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001

N;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AF0122
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A;Molecule type: DNA
A;Residues: 1-788 <KUI
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A; Gene: YPC
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                                                                                                  VNISAIEFRGQCLIERVRQALLVTGLPSHRLELEITERIMIEDADGALKIMTALKTLGIR
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EGIESEAQLQRLQKMGCHLGQGYFLTRPLPAEAM
                                 LSIDDFGTGYSSLNYLHRFPFDGLKIDKSFIDKLTESHEGQSIVEGIINLGHAISMTVIA
                                                                                                                                  VNISARQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQ
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29.1%; Pred. No. 2.
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A; Molecule type: DNA
A; Residues: 1-585 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB77743.1;
A; Cross-references: Strain PCC 7120
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.;
DNA Res. 8, 205-213, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein all0219 [imported] (Speciles: Anabaena sp. (Strain PCC 7120) C:Date: 14-Dec-2001 #sequence_revision C:Accession: AC1834
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C;Superfamily: hypothetical protein sll1895
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                              AQLORLORMGCHLGQGYFLTRPLPAEA 852
                                                                                        GTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESE
                                                                                                                          {\tt RFSQKKLLEDINQVLQDTGLDAQSLKLEITESVIMENGENATTMLNQLRNLGIELAIDDF}
                                                                                                                                            IVFPEEFMPIAQETGLIIPIDAWVLREACRQTRQWQEQIPSLSTDLHKQPLSISINLCSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYKPEELVGKNAFDFIHPDDITSNSQSFNYLIQNLGATVLVESRFRRKDGSWCFLESTGS 116
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EGVETAEQLTYLQSLHCDEVQGYFLAKPMPVEAL
                                                               GTGYSSLGRLHNFPINGLKIDQSFVSGRGVEAGNLHIVETIVTLSSKLGVDVTAEGVETP
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574
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14-Dec-2001 #text_change 11-Jan-2002
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M.; Yamada, M.; Yasuda, M.;
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RESULT

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conserved hypothetical protein PA3311 [imported] - Pseudomonas aeruginos C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2 C;Accession: B83232 C;R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.;
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Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas A;Reference number: A82950; MUID:20437337

A;Accession: B83232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-783 <STO>
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WAGKRGIDRRNILPRLSFEAWEETQKLVPTWNRSERKLAQVASTQLYMAITQ-QFVTRLI
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              EDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLSILKQLPIHRLKIDK
                                                                                                        GLINHLGQWVLETACATHQHFFRETGRRLRMAVNISARQFQDEKWLNSVLECLKRTGMPP
                                                                                                                                                            LDGRTLVMTASVGVSLYPNDGEQCEELLKNAGLALHQSKACGRNNAQFFSRQLLVRATQE
                                                                                                                                                                                                                                                    LQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDR
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                                                                     GMIDQLDDWVLRRACRDLRSLHLAGHERLRVAVNCCASNLGRASLVDEVRHALEQAGLAA
                                                                                                                                             LQMEEELRQALRDDQLELHYQPILALADGEVHQLEALVRWRHPTQGLLGPDRFIGLAEAN
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic A;Reference number: A82950; MUID:20437337

A;Accession: H83428
A;Status: preliminary
A;Molepule type: DNA
A;Residues: 1-685 <STO>
A;Cross references: GB:AE004599; GB:AE004091; NID:g9947702; PIDN:AAG05116.1; GSPDB:A;Experimental source: strain PAO1
C;GenetLos:
A;Genet PA1727
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EAQLQRLQKMGCHLGQGYFLTRPLPAEAMM 854
                                                        FGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIES
                                                                                              LQFAHAGLVDSVRNALLRHSLEPSHLILEVTESTAMRDADASLVILEQLSAMGVGISIDD
                                                                                                              RQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDD
                                                                                                                                                                    ERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEIALTRAKCQGKNTYQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAGRGID------NGWLAVLVIVITLAVIAIALIVSVLDSRLEAR-TSVLATSLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SILIAVIASGAALWIAFRLRHGSRRIVLVRAGAALVMGCAIVGMHYTGMAAAQFPLGSFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGTGYSSLLYLKRLPASELKIDRGFINELAHDSDDAAIVSAIVALGRTLNLKIVAEGVET
                                                                                                                                                     TPGQFLPLAEKTGLIVQIGEWVLDEAC------RQMRLWLDGGHADWNIAVNLSA
                                                                                                                                                                                                                                       YRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQV
                                                                                                                                                                                                                                                               EKLVKRISQPYQISRHEVRISASIGIALYPGDGQTRHELMINADAAMYHAKDQGRNGYCF
                                                                                                                                                                                                                                                                                                                       VNDAYGHHLGDLLLIEVAERIRANVRA----QDTIARLGGDEF-VLLIEAREPADAATLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tch 12.3%; Score 811; DB 2; al Similarity 34.4%; Pred. No. 6.3e-44; 196; Conservative 107; Mismatches 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004914; GB:AE004091; NID:g9951301; PIDN:AAG08402.1; GSPDB:GNA;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-899 <STO>
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Best Local
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EAQQEFLTRLGCNSLQGFLLGRPMPAEQLL
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160 RSQDDHLQHLLRSRTQQNLIVRLARHRYLSSDPLLEAAQLITQAACEAYGTARAGIWRLL
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                                             MGISTAPYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHHSKPRRFTEQEWETMALLSKEVS----LAITQSQLSRQVHQQQVQEALVQRLETTVAQ
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                                                                                                                                                                                                                                  IFNRQLTLALLDALYEG----KMVGVLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKL
IGLASAPQHGCDPQTLMKYAGLALHKAKANGKHQVQVFTEALTAEASYKLFVESNLRRAL
                                                                                                                                      SPLAAYSPLLSRWHGDGFTILL--TQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTAS
                                                                                                                                                                                      --NRHYFIGALEERLESSGDRPLSLLLVDIDNFKRINDSLGHQTGDKLLVSLARRLRSCL
                                                                                                                                                                                                                                                                                                                             SFEAWEETQKLVPTWNRSERKLAQVASTQLYMAITQQFVTRLITQQTAY-DPLTQLPNWI
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                                                                                                                                                                                                                                                                                                                                                                           -----RKNHEPY-----W-GQLSLSKVYDDLGELTHYIG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HLFQRAVEQSASAFLLIDRDGVVEYVNPSFT-SITQYSADEVR----NRRLSELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WQELMRGQPSAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDW
                                                                                           LARFASNEFAVLLDDTAVEKGES---IAAQVLHMLDKPLFVDNQLINITGS
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27.5%;
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Pred. No. 1.1e-43;
il; Mismatches 289;
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A;Molecule type: DNA
A;Residues: 1-687 <STO>
A;Cross-references: GB:AE004852; GB:AE004091; NID:g9950587; PIDN:AAG07755.1; GSPDB:GN00:
A;Experimental source: strain PAO1
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein PA4367 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83100
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Best Local Similarity
Matches 226; Conserv
467
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652 AQNELAVHYQPKLCLRSGQLLGLEALLRWQHPEKGMIRPDRFISVAEETGLIVPIGKWVI 711
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                                                    CLGLDDFKGINEQYTYQLGDQLLIALADRLRGHSARLGS----LARLGGDQFALVQADIE 341
                                                                                                                                                      VIAMDRFKRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDGFTILLTQIS 526
                                                                                                                                                                                                                                                                              ----LVYHWMLTKPLSK--IIEHLVSINPDRPSQHQLPLLKGHERNELGLWVTTANQLLA 230
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                                                                                                                                                                                                       SIESNSHLRREAEDNLLRISQYDFLTGLP-----NRQLLQQQLDQILDGAGRQQRRVAVL
                                                                                                                                                                                                                                          AITQQFVTRL----ITQQTAYDPLTQLPNWIIFNRQLTLALLDALYEG-----KMVGVL 466
                                                                                                                                                                                                                                                                                                                     KEKSLVKHWAGKRGIDRRNILPRL-SFEAWEETQKLVPT---WNRSERKLAQVASTQLYM 416
                                                                                                                                                                                                                                                                                                                                                          FSIRLIGRPPYSEYYGDLKITLD-TAP----YGENFVTTSEIIFISGILRALAMGLVLF- 176
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                                               QEAYIIAEGCNEGQGYLYSKPLPARELTQYL 672
                       QLQRLQKMGCHLGQGYFLTRPLPAEAMMTYL 857
                                                                                                                 FQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDDFG
                                                                                                                                                                                  WQHPRLGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRLRMAVNISARQ
                                                                                                                                                                                                            TRSRNRYQFYIASVDSEMRRRELEKDLRDALQRHELHLVYQPQVDYRDHRVVGVEALLR
                                                                                                     LHHNALPRVVSNLLQVYRLPARSLELEVTETGLMEDISTAAQHLLSLRRAGALIAIDDFG
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Search completed: June 7, 2002, 18:56:32 Job time: 206 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - protein search, using sw model
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Run on: June 7, 2002, 18:54:01 ; Search time 19.14 Seconds (without alignments) 2581.303 Million cell updates/sec

Title: US-09-272-809-2

Perfect score: 6614
Sequence: 1 MNPNRSLEDFLRNVINKFHR......GRNQWLAYEGSQLPHVDGEV 1276

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 105224 segs, 38719550 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

105224

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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adiantum ca	cucurbita p	oryza sativ	escherichia	ceratodon p	arabidopsis	arabidopsis	oryza sativ	pisum sativ	bacillus su	physcomitre	pinus sylve

ALIGNMENTS

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EGION. ind with the bilin tetrapy is shows red, far-red lights sphotochemically inactive D TETRAPYRROLE CHROMOPHORE	BIOCCHEMISTRY 39:13487-13495(2000). BIOCHEMISTRY 39:13487-13495(2000). -I- FUNCTION: PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE R FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE FRE FORM THAT	11063585; domain:	DOMAINS.	tochrome from Synechocystis sp. F	MEDIJINE-20435261; PubMed=10978170; Park CM., Kim JI., Yang SS., Kang JG., Kang JH., Shim JY.,	109-136(1996).	PCC6803. II. Sequence dete: ent of potential protein-co	"Sequence analysis of the genome of the unicellular cyanobacterium	Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Thimpo S.,	wa M., Sugiura M., Sasamoto S., Kimura T., Na Mirabi Nabarabi Nab	97061201; PubMed=8905231;	MORA ROME	92% of	p. strain PCC6803. I. Sequence feature	of the interlain	Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,	SEQUENCE FROM N.A. MEDITURE-06127500 Finhard-0500270	I_TaxID=1148;	. (strain PCC 6803).	CPH2 OR SLL0821.	st annotation update)	(Rel. 40, Creat	Q55434; STANDARD; PRT; 1276 AA.	E XNX.

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.erPro; IPR001294; Phytochrome.
.m; PF00563; EAL; 1.
.m; PF01590; GAF; 3.
.m; PF00990; GGDEF; 2.
.RT; SM000267; DUF1; 1.
.RT; SM00055; GAF; 3.
.RT; SM00065; GAF; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for comittees requires a license agreement (See http://www.isb-sib.ch/ansend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                              MNPNRSLEDELRNVINKEHRALTLRETLQVIVEEARIFLGVDRVKIYKFASDGSGEVLAE
KEKSLYKHWAGKRGIDRRNILPRLSFEAWEETQKLYPTWNRSERKLAQVASTQLYMAITQ
                                                                             YIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRGQPSAAMEPMAAVQSTWEKPRPFT
                                                                                                                                                          EVSLAITQSQLSRQVHQQQVQEALVQRLETTVAQYGDRPETWQYALETVGQAVEADGAVL
                                                                                                                                                                                                             GHYTTVDSCHIQYLLAMGVLSSLTVPVMQDQQLWGIMAVHHSKPRRFTEQEWETMALLSK
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cal Similarity 100.0%;
1276; Conservative
                                                                                                                     YIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRGQPSAAMEPMAAVQSTWEKPRPFT
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BILIN LYASE DOMAIN 2.

BILIN LYASE DOMAIN 2.

CHROMOPHORE 1 (PROBABLE).

C-SS: HOLOPROTEIN EXHIBITS NO PHOTOCHROMIC ACTIVITY.

H->F: CHROMOPHORE ILGATING ACTIVITY (IN VITRO) IS 30-40% LOWER THAN WILD-TYPE.

H->Q: CHROMOPHORE LIGATING ACTIVITY (IN VITRO) IS ABOUT 10% MORE EFFICIENT THAN WILD-TYPE.

WILLD-TYPE.

318CF3A7396ZD99E CRC64;
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SLL1895. Hypothetical

Synechocystis sp. (strain Bacteria; Cyanobacteria; Cyanobacteria;

Chroococcales;

Synechocystis

SEQUENCE FROM N.A. MEDLINE=97061201;

PubMed=8905231;

P74101; 01-NOV-1997 01-NOV-1997 16-OCT-2001

(Rel. (Rel. (Rel. 1 79.7

35, 40, kDa

, Created)
, Last sequence upo
, Last annotation of the protein sll1895.

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SMART; SM00262; DUF2; 1.
SMART; SM00091; PAS; 1.
SMART; SM00091; PAS; 1.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - i -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosouchi T., Matsuno A.,
Shimpo S., Takeuchi C.,
Tabata S.;
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Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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 QARCLYDLGCREMQGYWFSHPL-SEAEIT
                           QLQRLQKMGCHLGQGYFLTRPLPAEAMMT 855
                                                    TGYSSLSYLKTPPFNTLKIDRSFTKDILHTPKDAAIIQAMLLLGNGFNLNIIAEGIEEEP
                                                                     TGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEA
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Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumu
akeuchi C., Wada T., Watanabe A., Yamada M., Yasuda
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38.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 821.5; DB 1
Pred. No. 1.1e-45;
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78EB2D4A0EAF6801 CRC64;
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682
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184;
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nura T.,
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OF P5552

DT 01-NOV

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Best Local
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Pfam; PF00990; GGDEF; 1.
Pfam; PF00990; GGDEF; 2.
Pfam; PF00989; PAS; 3.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
SMART; SM000085; PAC; 2.
SMART; SM00091; PAS; 3.
PROSITE; PS50113; PAS; 2.
PROSITE; PS50113; PAC; 2.
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
SEQUENCE
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P55552;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMA I N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000160; DUF9.
InterPro; IPR001610; PAC.
InterPro; IPR000700; PAS-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commarcial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000014; PAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000083; AAB91764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of symbiosis between Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
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MEDLINE-97305956; PubMed-9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae;
                                                                                          102
                                                                                                                                                                                   62
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    PSGEVLEIGPRWEKTGYAPKEALGA----
                                         ----VAQYGDRPETWQYA-LETVGQAVEADGAVLYIAPDLTGSVAQHYQWNLRFDWGNWL
                                                                                                                                TEQEWETMALLSK-----EVSLAITQSQLSRQVHQQQVQE----
                                                                                                                                                                                                                        ISPTEHSNGHYTTVDSCHIQYLLAMGVLS----SLTVPVMQDQQLWGIMAVHHSKPRRF
                                                                                      VTR--KSRAILTRGSSSEKVIVAIALDVTECRTAEAALQASVEHHRSLTELHPQVPWTAD
                                                                                                                                                                              ILPTAEAD-RYRDMD-----IGVLSTGEEVSVEEPI-----
                                                                                                                                                                                                                                                                       al Similarity
235; Conserv
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265
338
827 ;
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B kDa protein )
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PAS-assoc_C.
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Last annotation update)
protein Y4LL.
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                                                                                                                                                                                                                                                                       127;
                                                                                                                                                                                                                                                                                                                                                                                    MW;
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PAC 1.
PAS 2.
PAS 2.
PAC 2.
PAC 2.
W; OD6CBF1142027FAB CRC64;
                                                                                                                                                                                                                                                                    Score 708; DB 1;
Pred. No. 3.5e-38
77; Mismatches 31
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    -GWAKAMHPDDLGEVQR---
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                                                                                                                                                                                                                                                                                                              Length 827;
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                                                                                                                                                                                                                                                                    Indels 140;
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                                                                                                                                ALVORLETT --
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EWAKSL
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Aiba
                                                                                                     SEQUENCE FROM N.A.
STRAII-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                PDDU_ECOLI STANDARD; PRT; 7
P76129; P7708; P76872;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Hypothetical protein yddU.
            MEDLINE=97251357;
                           STRAIN-K12;
                                                                                                                                                                                                                         Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                 ECOLI
                                                                                                                                                                                                                 Escherichia
                                                                                          Mau B., Shao Y.;
                                                                                                                                                                                                   NCBI_TaxID=562;
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                                      EQUENCE FROM N.A.
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H.,
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                                                                 complete genome sequence ce 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWLNAVHPDDRNAVERVFYQAFDLREPV-----RMEYRLKRAGGGSAWVIDIGQPRFASD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRSDWIAPPESLSAENFQSFLIVPLAADQQWV-----GSLILLR-----KEKSLVK
                                                                                                                                                                                                                                                                                                                                                                                                     TVEGVERQDQLDTIKAEGFDEAQGYLFGGPLPASQAMALL
                                                                                                                                                                                                                                                                                                                                                                                                                            VAEGIESEAQLQRLQKMGCHLGQGYFLTRPLPAEAMMTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIVAIDDFGTGYSSLSYLRTFPFDKIKVDRSFIADLPKSKESLAIVRAVAAIGRSLGIIT
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 Baba
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PubMed=9097039;
Fujita K., Haya
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Hayashi
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                                                                              Escherichia
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J91; BAA151.

J92; BAA151.

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ro; IPR00163; DUF2.

Pro; IPR001610; PAC.

LerPro; IPR001610; PAC.

LerPro; IPR001610; PAC.

LerPro; IPR001614; PAS.

Pfam; PF00990; GGDEF; 1.

Pfam; PF00990; GGDEF; 1.

Pfam; PF00989; PAS; 2.

SMART; SM00052; DUF1; 1.

LR SMART; SM00052; DUF2; 1.

DR SMART; SM00086; PAC; 2.

PROSITE; PS50112; PAS; 2.

PROSITE; PS50112; PAS; 2.

PROSITE; PS50113; PAC; 1

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DOMAIN
SEQUENCE
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-I- SIMILARITY: BELONGS TO THE YEGE/YHDA/YHJK/YJCC FAMILY.
-I- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION
-I- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
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EMBL; D90789; BAA15144.1; -.
EMBL; D90790; BAA15154.1; -.
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PROSITE; PS50113; PAC; 1.
Hypothetical protein; Repeat; Complete DOMAIN 10 79 PAS 1.
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Laboratory strains.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ datab
-!- SIMILARITY: BELONGS TO THE YEGE/YHDA/YHJK/YJCC
-!- SIMILARITY: SOME, TO SYNECHOCYSTIS SP. SLR0359.
              InterPro;
InterPro;
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

STRAIN-CDC 1, Alland D., Eisen J.A., Carpenter L., White O., Fléischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YD54_MYCTU
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NCBI_TaxID=1773;
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een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no restr
                                                 ; AE007012; ; P03622; 2II; MT1397; -.
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7 OR MTCY02B10.18C.
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STRAIN=K12 / MG1655;
STRAIN=F12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
Riley M., Davis N.W., Kirkpatrick H./
                                                                                                                                                                                                YCIR_ECOLI
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01-NOV-1997
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Pfam; PF00990
SMART; SM0026
SMART; SM0006
SMART; SM0006
Hypothetical
SEQUENCE 62
            Gregor J., Davis N.W., Mau B., Shao Y.;
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16-OCT-2001
                                                                                                                                                   YCIR OR B1285
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1590; GGDEF; 1.

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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SMART; SM00267; DUF1; 1.
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SMART; SM00091; PAS; 1.
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STRAIN-K12 / MG1655;
MEDLINE-94316500; PubMed-8041620;
Sofia H.J., Burland V., Daniels D.L., Plumandlysis of the Escherichia coli genome.
"Analysis of the Escherichia coli genome."
  Complete proteome.
SEQUENCE 651 AA:
                                              Pfam; PF00672; HAMP;
SMART; SM00267; DUF1;
SMART; SM00052; DUF2;
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Query Match

8.5%;

Score 561; DB 1; pred. No. 8.6e-29;

Length 651; Indels

94;

Gaps

17;

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                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 80.5 kDa protein in ntrC 5'region (ORF1).
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                                                                                                                    STRAIN-UKS5/1;
MEDLINE-92092954; PubMed=1661370;
MEDLINE-92092954; PubMed=1661370;
Pawlowski K., Klosse U., de Bruijn F.J.;
"Characterization of a novel Azorhizobium caulinodans ORS571
"Characterization of a novel Azorhizobium caulinodans ORS571
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component regulatory system, NtrY/NtrX, and metabolism.";
Mol. Gen. Genet. 231:124-138(1991),
MOI. GEN. GENET. 231:124-138(1991),
MOI. GEN. GENET. 231:124-138(1991),
MOI. GEN. GENETARNY: CONTAINS 1 PAS (PER-ARNY)
                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Hyphomicrobium group; Azorhizobium.
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           YEGE/YHDA/YHJK/YJCC FAMILY.
(PER-ARNT-SIM) DIMERIZATION DOMAIN
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Best Local Similarity
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SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
SMART; SM00065; GAF; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical | DOMAIN 1: DOMAIN 2 SEQUENCE 73
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InterPro; IPR001610;
InterPro; IPR000700;
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PF01590; GAF; 1.
PF00990; GGDEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                          VLYIAPDLTGSVAQHYQWNLRFDWGNWLETSLWQELMRGQPSAAMEPMAAVQSTWEKPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                              AFKCIAAVLAGLLARSGTEGLVSEAARRAM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEVSLAITQSQLSRQVHQQQVQEALVQRLETTVAQYGDRPETWQYALETVGQAVEADGA 238
                                                                                                                                                                                                                                                                                            FTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAENFQSFLIVPLAADQQWVGSLIL
                                                                                                                                                                                              LRKEKSLVKHWAGKRGIDR----RNILPRLSFEAWEETQKLVPTWNRSERKLAQVASTQLY
                                                                                                                                                                                                                                             GVIGRPMTET-IIPAHYIDRHRQGFMRHLATGENHIMRRLVE--VEALRAD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221;
                                                                                                                                                  FPAELTVNEHRAGGRRLFSAFVRDISDRIT---
RINESFCHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDGFTILLTQISDNQEMIPL 534
                                                 TGLSNRTGLLRLCTGRPT-
                                                                                             MAITQQF-VTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALYEGKMVGVLVIAMDRFK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50112; PAS; 1
PS50113; PAC; 1
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IPR000014; PAS
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1 protein.
185 2;
263 3
735 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GVVTFLTEPVMVHGRWWG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 F
313 F
80476 MW;
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DUF9
GAF.
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24.7%;
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Pred. No. 5.2e-27;
25; Mismatches 338
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PAC:
CFF94DDF06440B9A CRC64;
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                                                                 -RPSGAVVLMLRDLG
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YJCC_ECOLI
P32701; P76789;

01-0CT-1993 (Rel. 27, Created)

1 01-NOV-1997 (Rel. 35, Last sequence update)
1 01-MAR-2002 (Rel. 41, Last annotation update)
"""nothetical protein yjcC.
          Query Match
Best Local :
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _ECOLI
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=94089392; PubMed=8265357;
Blattner F.R., Burland V.D., Plun
                                                   EcoGene; EG11938, yjcc.
InterPro; IPR001633; DUF2.
Pfam; PF00563; EAL; 1.
SMART; SM00052; DUF2; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete Pf6E4819954912F31 CRC64;
                                                                                                                                                                                                                                          "Analysis of the Escherichia coli genome. IV. DNA sequence region from 89.2 to 92.8 minutes.", Nucleic Acids Res. 21:5408-5417(1993).
-i- SIMILARITY: BELONGS TO THE YEGE/YHDA/YHJK/YJCC FAMILY.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                        EMBL; AE000479; AAC77031.1;
                                                                                                                                 EMBL; U00006; AAC43155.1; -.
                                                                                                                                                                                                                                                                                      Daniels D.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AETLIGRLRSAIESGGRRFYLRVGLGVVERPGD---ATYLLRDAEMA--ARDCRDGHLLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YSSLSYLQRLPMDVLKIDRSFVLDMVDNSRSREIVRVMIEMAHGLGMSVVAEGVETTGAL
94;
           Similarity
 Conservative
          6.0%;
                                                                                                                                                                                                                                                                                                                                                                          gamma
  60;
Score 400; DB 1;
Pred. No. 1.8e-18;
0; Mismatches 99
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                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                  Sofia
                                                                                                                                                                                                                                                                            DNA sequence
                     Length 528;
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            EMBL; D90721; BAA35528.1;
EMBL; D90722; BAA35536.1;
EcoGene; EG13476; YliE.
                                             EMBL;
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RESULT 10
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16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Hypothetical protein yllE.
YLIE OR B0833.
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P75800;
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Mayhew G.F. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                              Yano M., Horiuchi T.;
7A 718-kb DNA sequence of the Escherichia
corresponding to the 12.7-28.0 min region
DNA Res. 3:137-155(1996).
-!- SIMILARITY: CONTAINS 1 DUF2 DOMAIN.
                                                                                                                                                                                                                                                                                                                MEDLINE-97061202; PubMed-8905232;
OShima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Ikemoto K., Inada T., Itoh T., Kasjihara M., Kinura S., Miki T., Mizobuchi K.
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mau B., Shao Y.;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                            between
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                                                                       SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the Ex
European Bioinformatics Institute. There are no restr
by non-profit institutions as long as its content
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AE000185; AAC73920.1;

IPR001633;

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Best Local Sin
Matches 130;
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P77172;
       Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00563; EAL; 1.
SMART; SM00052; DUF2; 1.
Hypothetical protein; Complete
DOMAIN 526 772
ECQUENCE 782 AA; 90048 MW;
                                       STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
                                                                                                      Escherichia
                                                                                                                             Escherichia coli.
                                                                                                                                          Hypothetical
YFGF OR B2503
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
                                                                     SEQUENCE
                                                                                          NCBI_TaxID=562;
                                                                                                                 Bacteria; Proteobacteria;
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22.6%;
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Best Local Similarity
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Pfam; PF00563; EAL; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
Hypothetical protein; Complete p:
DOMAIN 492 736 DUF:
SEQUENCE 747 AA; 85607 MW; 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamagata S., Horiuchi T.;

'Construction of a contiguous 874-kb sequence

'Kl2 genome corresponding to 50.0-68.8 min on
analysis of its sequence features.";

DNA Res. 4.91-113(1997).
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STFQEPFFLQGQPIYLTASMGIS----TAPYD-----GETAESLLKFAEIAL-TRAKCQ
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                                                                             MKGENDELISPDSFLPVAHEFGLSSSIDMWVIEHTL----QFMAENRAKMPAHRFAINLS
                                                                                                               WQHPRLGQVAPDVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRL---
                                                                                                                                                                                         MQRRGAMYLQRE---LKDKVAMMNRLQQALEHNHFFLMAQP-
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg the Colonay M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 33.9 kDa protein Rv1357c.
RV1357C OR MT1400 OR MTCY02B10.21C.
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Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Corvnebacterineae; Mycobacteriaceae; Mycobacterium.
Pfam; PF00563; EAL; 1.
SMART; SM00052; DUF2; DU
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE YEGE/YHDA/YHJK/YJCC FAMILY.
                                                                                                                                                                                                                                                                                                                           EMBL; AE007012; AAK45663.1; TIGR; MT1400; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole genome comparison of Mycobacterium tuberculosis clinical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation
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STRAIN=K12 / MG1655;

STRAIN=97456617; PubMed=9278503;

Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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EMBL; U82664; AAB40212.1; ALT_INIT.
ECOGENE; EC14237; ylaB.
InterPro; IPR001633; DUF2.
Pfam; PF00563; EAL; 1.
SMARR; SM00052; DUF2; 1.
SMARR; SM00052; DUF2; 1.
SMARR; SM00052; DUF2; 1.
Complete TRANSMEM 6 26 POTENTIAL.
TRANSMEM 6 262 POTENTIAL.
                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Dav Roberts D., Federspiel N., Hyman R., Kalman S., Komp C., Kuj Duncan M., Federspiel N., Oefner P., Schramm S., Davis R.V Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.V Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

-i- SIMILARITY: BELONGS TO THE YEGE/YHDA/YHJK/YJCC FAMILY.
                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                  complete genome sequence nce 277:1453-1474(1997).
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35.9%;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K. Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K. Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
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                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                 "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch
Riley M., Collado-Vides J., Glasner J.
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           Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., In Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makin Mizobuchi K., Mori H., Mori T., Motomura K., Nakade Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei Sivasundaram S., Tagami H., Takeda J., Takemoto K., Yamamoto Y., Horiuchi T.;
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SMART; SM00052; DUF2; 1.
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EMBL; D90751; BAA36004.1; ALT_INIT.
ECOGENE; EG13888; YCGG.
InterPro; IPR001633; DUF2.
                                                                                                         STRAIN-K12;
MEDLINE-97251358;
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                                                                                                                                     SEQUENCE
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MEDLINE=97426617; PubMed=9278503;
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                                                                                                         PubMed=9097040;
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Last annotation updat
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Pred. No. 5
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.9e-16;
coli K-12 on the lin
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                                                  ni K., Inada T., Iso
1., Makino K., Miki
Nakade S., Nakamura
Sampei G., Seki Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.4%; Score 358.5; DB 1; Length 532; Best Local Similarity 32.6%; Pred. No. 9.2e-16; Matches 89; Conservative 55; Mismatches 100; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000276; AAC74885.1; ALT_INIT.
EMBL; D90825; BAA15622.1; ALT_INIT.
EMBL; D90826; BAA15627.1; -.
ECOGENE: EG13516; yoab.
InterPro; IPR001633; DUF2.
Pfam; PF00553; EAL; 1.
SMART; SM00052; DUF2; 1.
Hypothetical protein; Complete proteome.
DOMAIN 265 507 DUF2.
SEQUENCE 532 AA; 59711 MW; 977155A7D56C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: CONTAINS 1 DUF2 DOMAIN.
         492
                                                                                                                                                               667 IGLINHLGQWVL-ETACATHQHFFRETGRRLRMAVNISARQFQ------DEKWLNSVL 717
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                                                                                                                                                                                                                                                                                                                                                     -----HPIQQLILETTERDALLDVDYRIA--RELHRKNVKLAIDDFGTGNSSFSWLET 431
ILOGYLYAQPMPLRD-----FPKWLAGSQPPP 518
                                                                                 LGQGYFLTRPLPAEAMMTYLYYPQILDFGPTPP 870
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Search completed: June 7, 2002, 18:58:02 Job time: 241 sec

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Database :
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Listing first 45 summaries
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1 MNPNRSLEDFLRNVINKFHR......GRNQWLAYEGSQLPHVDGEV 1276
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Gapop 10.0 , Gapext 0.5
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: sp_phage:*
): sp_plant:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result No.
774.5	780.5	785	789.5	797	801.5	809	810.5	811	811.5	830.5	858.5	862.5	865	882	922	Score
11.7	11.8	11.9	11.9	12.1	12.1	12.2	12.3	12.3	12.3	12.6	13.0	13.0	13.1	13.3	13.9	Query Match Length
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Q98g38 rhizobium l	Q981y4 rhizobium 1	Q984y8 rhizobium l	Q914f1 bacillus ce	P74400 synechocyst	P72843 synechocyst	Q9hw35 pseudomonas	Q9huf2 pseudomonas	Q9i310 pseudomonas	Q9hyt3 pseudomonas		Q92kj3 rhizobium m		Q55576 synechocyst	Q9a3v7 caulobacter	Q9hvi8 pseudomonas	Description

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08/3/8 acetopacter	_		2	S		Q9htq9 pseudomonas	Q971d1 clostridium		P72746 synechocyst	Q9k8n4 bacillus ha	087376 acetobacter	Q9z584 streptomyce	Q9abx9 caulobacter	034311 bacillus su	Q9rx49 deinococcus	Q92yn0 rhizobium m	Q930x2 rhizobium m	Q92wb4 rhizobium m	Q9aa66 caulobacter		S			Q9rs28 deinococcus	(J)	~	Q9htc4 pseudomonas	Q98jq6 rhizobium l

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Best Local S
Matches 250
        O9A3V7, PRELIMINARY; PRT; 748 AA.
O9A3V7, 101-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SENSORY BOX/GGDEF FAMILY PROTEIN.
CC3094.
Caulobacter crescentus:
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 Bacteria;
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Proteobacteria;
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Pred. No. 4.3e-55;
2; Mismatches 263
subdivision;
Caulobacter
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group;
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Matches 203
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Pfam; PF00590; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
SMART; SM00051; PAS; 1.
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Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White (Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M., "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL, AE005972; AAK25056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome SEQUENCE 748 AA
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STRAIN=ATCC 19089
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NCBI_TaxID=69394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                      NSVLECLKRTGMPPEDLELEITESLAMEDIKGTVVLLHRLREEGVQVAIDDFGTGYSSLS
                                                                                                                                                                                                            MGCHLGQGYFLTRPLPAEAMMTYLYY---
                                                                                     YLRSFPFDKIKIDQTFVRDILHDSDAMAIIKAVLDLGASMGVVTTAEGVETQAQLDALRQ
                                                                                                                                         RTVVSALAASGLPAQRLELEITESVLLQDSQANMIMLHDLKALGVRISMDDFGTGYSSLS
                                                                                                                                                                                               MVSPADFIPLAEEIGLIVQLGEWVLRRACAEAANW----PEHVRLAVNLSPAQFRDRGLV
                                                                                                                                                                                                                                                      HFFERAMDEQLQARRALELDLRRALQAGEFELFYQPLYHLGDERVTGCEALLRWRHPERG
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                               QGCAEIQGYFISRPAPASEIAKMLGVEGRADLGAPSVLSPIGANPPPPQ-AGQEVRTAPS
                                                                                                              ILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQK
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IPR000700; PAS-assoc_C
0563; EAL; 1.
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IPR000160; DUF9.
    EAGQGNVG
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                                                         POILD-FGPTPPLPKVALPETET---
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Hypothetical
SEQUENCE 12
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Q55576;
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InterPro;
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"Sequence analysis of the genome of t
Synechocystis sp. strain PCC6803. I.
region from map positions 64% to 92%
DNA Res. 2:153-166(1995).
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Synechocystis sp. (strair
Bacteria; Cyanobacteria;
NCBI_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                          SMART;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 141.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                               SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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KYRYIVELTSEGIWILDQDQQTTFANQQLADMLGYSVQEILEKNITAFYLVIHHLPESQN
                                                                                IPFVADQATEITLTPLDGSMVVAEMRVSPIHWQKGKAFLVSLRDITEQHQARLALAESEK
                                                                                                                                                                                                                                                                                                                  PF00785; PAC; 4.
PF00989; PAS; 3.
; SM00267; DUF1; 1.
; SM00052; DUF2; 1.
; SM00065; GAF; 1.
; SM00086; PAC; 4.
; SM00091; PAS; 4.
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                                                                                                                                                                                       Similarity
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IPR000160; DUF9.
IPR003018; GAF.
IPR001610; PAC.
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1244 AA;
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31.0%;
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                                                                                                                                                             Score 865; DB
Pred. No. 3.3e
41; Mismatches
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% of the genome.";
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.3e-51;
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aruo K., Okumura
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01-MAR-2001
01-DEC-2001
    SEQUENCE FROM N.A.

SETRAIN-ATCC 15692 / PAO1;

MEDLINE-20/437337; PubMed-10984043;

MEDLINE-20/437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren H.Ckey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., La Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yu Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Saier M.H., Hancock R.E.W., Low, Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lorshopmana PAO1, an
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 genome
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SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
SMART; SM00095; PAC; 3.
SMART; SM00091; PAS; 4.
SMART; SM00062; PBPb; 1.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              opportunistic pathogen."; Nature 406:959-964(2000).
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                                                                                                                                                                LPNWIIFNRQLTLALLDALYEGKMVGVLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQ 498
                                                                                                                                                                                                                                                                                                                                         LMRGQPSAAMEPMA---AVQSTWEK----PRPFTSVAPLPPTNCVPHGYTLGELEQRSDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIGIAADDAIGKTA--TELGI-WALPGLGPQVLEKLGH-GNLTNLEVPLRRRNGSTFSAL
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                                        VGIALFPKDGDDAPTLVKNADAAMYRAKSRGRSRIEYYTRELTYLATERMALETELRRAL
                                                     MGISTAPYDGETAESLLKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQAL
                                                                                              QLRDV----DTVARLGGDEFIILLPGLHQESDAEHVARKLLNAFTAPFQADGHEFFVSAS
                                                                                                                       KLSPLAAYSPLLSRWHGDGFTILLTQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTAS
                                                                                                                                                   LPNRLLFESRLNHALDEAREESRPGAVLFIDLDRFKHINDSLGHPIGDLLLKAIAERLRD
                                                                                                                                                                                                       LTISAVHNPQGEITHFVGVFADISTLKYAQAR----
                                                                                                                                                                                                                               LSFEAWEETQKLVPTW-----NRSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQ
                                                                                                                                                                                                                                                                                     IAPPESLSAENFQSFLIV----PLAADQQWVGSLILLRKEKSLVKHWAGKRGIDRRNILPR
                                                                                                                                                                                                                                                                                                              KLQ-QAATVFESTAEGVMITDTRORITAVNRAFSEIT-----GYS----EQEALG
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GGDEF;
PAC; 3
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139659 MW; F483F0AD326C0FCB
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SBP_bac_3.
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Mismatches 345;
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Best Local S
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EMBL; AL591785; CAC45531.1; -
Hypothetical protein; Complete proteome.
SEQUENCE 772 AA; 85457 MW; 2856FE32277632C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O92KJ3 PRELIMINARY; PRT; 772 AA.

O92KJ3; PRELIMINARY; PRT; 772 AA.

O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe
Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti). Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Sinorhizobium.
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FTILLTQISDNQEMI-PLCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLK
                                                                                                                                                                                                                                                   WNRSERKLAQVASTQLYMAITQQFVTRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALY : :::| :|: :| :| :| :| :: :|: :: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: 
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                                                                                   ERDQWAYLAFLDLDDFKLINDSLGHATGDELLKIVAGRMRAAV----RRSDSVVRVGGDE
                                                                                                                                                                                                                  PSEQQQELIAMAAHLAGIAIERKRAEDRIGFMAHHDALTGLPNRVLFEEQVA-GMLEEIR
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38.2%;
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Pred. No. 4.4e-51
8; Mismatches 19
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2 STRAIN-ATCC 15692 / PAO1;

2X MEDLINE-20437337; PubMed=10984043;

3X MEDLINE-20437337; PubMed=10984043;

3X Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

3X Alickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

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3X Alickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Hufnagle W.O., Kowalik D.J., Lagrou M.,

3X Alickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Hufnagle W.O., Kowalik D.J., Hufnagle W.O., Kowalik D.J., Hufnagle W.O., Kowalik D.J., Hufnagle W.O., 
                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00990; GGDEF; 1.
Pfam; PF00989; PAS; 1.
Pfam; PF00989; PAS; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
SMART; SM00098; PAC; 2.
SMART; SM00091; PAS; 2.
Hypothetical protein; Complete p.
SEQUENCE 760 AA; 86380 MM; 0.
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InterPro; IPR000160; DUF9.
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   LWQELMRGQPSAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQ------
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                                                             ELGDPIETWKKRLHPEEYATVLEAHRNHL - - - QGLTDNLDHIYR - - LRHKDGDYRWIHS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAETALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTG
                                                                                                                                                                                                al Similarity
238; Conser
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IPR000014; PAS.
IPR000700; PAS-assoc_C.
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33.3%;
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Last annotation updat
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Pred. No. 3.
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049AFD1D6E222E05
                                                                                                                                                                                                Mismatches
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                                                                    HQDQALFLREHGCDFGQGYWYGRPQPAEALRF------DLPPVALPE
                                                                                                                       DFGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIE
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PRT;
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 15692 / PAO1;

RX MEDLINE-20437337; PubMed-10984043;

RX MEDLINE-20437337; PubMed-10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Brody L.L., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

RT Opportunistic pathogen.";

RI Nature 406.959-964 (2000).

DR EMBL; AE004753; AAG06699.1; -.

DR InterPro; IPR00163; DUF9.
                                         Q9HYT3;
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
HYPOTHETICAL PROTEIN PA3
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Bacteria; Pi
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N PA3311.
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Lagrou M., Yuan Y., Lim R.M., ס

Salte Barner, Long, a.

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Best Local Similarity
Matches 239; Conserv
Q9I310
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Hypothetical protein; Complete prot
SEQUENCE 783 AA; 86815 MW; 7D88
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Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
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                                                                                        SEVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIESEAQLQRLQKMGCHLGQGYFLTRP
                                                                                                                                 CFLELEVTEDALMYNIDQTIPLLERLRELGVSLSIDDFGTGYSSLAYLRRLPLDALKVDR
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                                                  LPLAALEEFL --
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PRELIMINARY;
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PRT;
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7D881B379356430F CRC64;
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RP SEQUENCE FROM N.A.

RC STRAIN-ANCC 15692 / PAO1;

RX MEDLINE-20437337; Pubmed-10984043;

RX Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

RA Brody L.L., Coulter S.N., Folger K.R., Was A., Larbig K., Lim R.M.,

RA Brody L.L., Coulter S.N., Folger K.R., Wa Z., Paulsen I.T.,

RA Brith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

"Proportunistic pathogen.";

RI Nature 406:959-964(2000)

DR EMBL; AEO0459; AAG05116.1;

DR SWART; SM00267; DUF2; 1.

DR SWART; SM00267; DUF2; 1.
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01-mar-2001 (TrEMBLrel. 16, Cr
01-mar-2001 (TrEMBLrel. 16, La
01-DEC-2001 (TrEMBLrel. 19, La
HYPOTHETICAL PROTEIN PA1727.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
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FGTGYSSLLYLKRLPASELKIDRGFINELAHDSDDAAIVSAIVALGRTLNLKIVAEGVET
                                                   FGTGYSSLSILKQLPIHRLKIDKSFVNDLLNEGADTAIIQYVIDLANGLNLETVAEGIES
                                                                                                                                                                                                                                                   RQFQDEKWLNSVLECLKRTGMPPEDLELEITESLMMEDIKGTVVLLHRLREEGVQVAIDD
                                                                                                                                                                                                                                                                                                                                                                                                     TPGQFLPLAEKTGLIVQIGEWVLDEAC-
                                                                                                                                                                                                                                                                                                                                                                                                                                              APDVFIPLAEELGLINHLGQWVLETACATHQHFFRETGRRLRM------AVNISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FESSMNANAQEQLQLLHDLRQALERRQLVLHYQPKVLAPNGPMIGVEALLRWEHPQHGLI 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRPQDSAPMLDRLTLESDLRQALTNQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQV
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                                                                                                                                                                                                     LQFAHAGLVDSVRNALLRHSLEPSHLILEVTESTAMRDADASLVILEQLSAMGVGISIDD
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Best Local Similarity
Matches 248; Conserv
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SMART; SM000267; DUF1; 1.
SMART; SM00005; DUF2; 1.
SMART; SM00065; GAF; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 1.
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Q9HUF2;
Q1-MAR-2001 (TIEMBLIEL 16, C
Q1-MAR-2001 (TIEMBLIEL 16, L
Q1-DEC-2001 (TIEMBLIEL 19, L
HYPOTHETICAL PROTEIN PA5017.
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SMART; SM0009
Hypothetical
SEQUENCE 89
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O.; Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
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Pfam; PF00990; GGDEF;
Pfam; PF00785; PAC; 1
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InterPro;
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
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NAQRDPRTQEL----
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EAQQEFLTRLGCNSLQGFLLGRPMPAEQLL
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IPR000014; PAS.
IPR000700; PAS-
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899 AA; 1
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AA; 101321 MW; 925C1FA936731602 CRC64;
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Last annotation updat
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Pred. No. 1.3e-47;
1; Mismatches 289;
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DR E	RT	RT	RA	RA PA	RA A	RX	RC	RP A	2 X	00	8	SO	GN			D F			RESULT 09HW35	рь	VΥ	}	Db .	Qy	Db	Ķ	Q	Db	Оy	5	子	Qу	Db	Qy	Д	: 5	ΟV	Db	Ωу	Db	Qy	Ф	ξŠ	•	рь	Qy
Nature 406:959-964(2000). EMBL: AE004852: AAG07755.1:	opportunistic pathogen.";	<pre>"Complete genome sequence of Pseudomonas aeruginosa PAO1, an</pre>	?	A Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,	Hickey M.J., Brinkman F.S.L., Biwin A.L., Mizogueni S.D., Warrener P.,	5	STRAIN-ATCC 15692 / PAO1;	SEOUENCE FROM N.A.	NCBI_TaxID=287;		Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;	onas aeruginosa		PROTEIN PA4367.	(Tremburel, 18,	(Tremblice) 16. Last segmence undate	7	Q9HW35 PRELIMINARY; PRT; 687 AA.	10	892 RYP 894	858 XXP 860		832 DMEITSAVIAMAHNLKLKVVAEGVESAEQLAFLRRNRCDIGQGYLFDRPIPSDLLNTSLL 891 -	799 DTAIIQYVIDLANGLNLETVAEGIESEAQLORLOKMGCHLGQGYFLTRPLPAEAMMT-YL 857	772 LLDATDDTRQQLERLKSLGLTLAMDDFGTGYSSLSYLKKFPIDVIKIDRSFIKDIPDSQD 831		730 MMEDIKGTVVIIHBIBEEGVOVATINEGERGVSSTSTIKOIBIBIKINKSEVNIIINEGA 708	712 REACROARELAEAGLGELQIAINLSPKQFTDPDLVGSIAAILHEENIPASQLELELTESL 771	679 ETACATHQHFFRETGRRLRMAVNISARQFQDEKWLNSVLECLKRTGMPPEDLELEITESL 738	24 OKNOBO ANTRE ARCHAOGRAFIO REPORTANTAL DATA TO AUGUSTALIDADA SERVICIONAL SERVICIONAL DE CONTRACTOR DE L'ORDANTAL DE L'ORDANT	652 ADMRTAVHYODKTOTRAGOTTATTATTATTATTATTATTATTATTATTATTATTATTA	619 TNQEFVLYFQPQVALDTGKLLGVEALVRWQHPRLGQVAPDVFIPLAEELGLINHLGQWVL 678	592 IGLASAPQHGCDPQTLMKYAGLALHKAKANGKHQVQVFTEALTAEASYKLFVESNLRRAL 651	559 MGISTAPYDGETAESILKFAEIALTRAKCQGKNTYQFYRPQDSAPMLDRLTLESDLRQAL 618	539 GDGATLARFASNEFAVLLDDTAVEKGESIAAQVLHMLDKPLFVDNQLINITGS 591		501 SPLAAYSPILSRWHGDGFTILLTOISDNOEMIPICERLLSTFOEPFFLOGOPIYLTAS 558	481NRHYFIGALEERLESSGDRPLSLLLVDIDNFKRINDSLGHQTGDKLLVSLARRLRSCL 538	444 IFNRQLTLALLDALYEGKMYGVLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKL 500	453 480	385 SFEAWEETQKLVPTWNRSERKLAQVASTQLVMAITQQFVTRLITQQTAY-DPLTQLPNWI 443	425 RKNHEPY W-GQLSLSKYYDDLGELTHYIG 452	LAPPESI		396 ALENLSELLFDARSALTQQNSWQ	271WQELMRGQPSAAMEPMAAVQSTWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDW 326

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Best Local Similarity
Matches 226; Conser
                                        P7.843;
P7.843;
P7.843;
O1-FEB-1997 (TrEMBLrel. 02, L:
O1-FEB-1997 (TrEMBLrel. 02, L:
O1-DEC-2001 (TrEMBLrel. 19, L:
O1-DEC-
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InterPro; IPR000160; DUF9.
Pfam; PP00563; EAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00257; DUF1; 1.
SMART; SM00525; DUF2; 1.
Hypothetical protein; Complete p:
SEQUENCE 687 AA; 77564 MW; 44
  SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGYSSLSYLKSLPLDKIKIDKSFVQDLLQDEDDATIVRAIIQLGKSLGMQVIAEGVETAE
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, Last annotation update
ACTIVATOR PROTEIN.
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No. 1e-47;
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Pfam; PF00072; response_reg; 1
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
SMART; SM00096; PAC; 2.
SMART; SM00091; PAS; 2.
SMART; SM0009448; REC; 1.
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InterPro;
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Miyajima N., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Yamada M., Yasuda M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicel Synechocystis sp. strain PCC6803. II. Sequence entire genome and assignment of potential protections. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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nes 234; Conserv
                                                                       KMVGVLVIAMDRFKRINESFGHKTGDGLLQEVADRLNQKLSPLAAYSPLLSRWHGDGFTI
ILDQVSHSRKLMAIAQRLLRVMRQPVNLQGLEFFVHGSIGITVFPDDGFHADVLLRNADT
                            LLTQISDNQEMIPLCERLLSTFQEPFFLQGQPIYLTASMGISTAPYDGETAESLLKFAEI
                                                        HIFGLMFLDLDNFKKVNDTLGHDAGDQLLVEVSERLQRAL----RQTDTVARLGGDEFLI
                                                                                                                                LAQVASTQLYMAITQQFV----TRLITQQTAYDPLTQLPNWIIFNRQLTLALLDALYEG
                                                                                                                                                                                                   LAADQQWVGSLILLRKEKSLVKHWAGKRGIDRRNILPRLSFEAWEETQKLVPTWNRSERK 405
                                                                                                                                                                                                                                 DVQGNITYVNPK-FEEIS--
                                                                                                                                                                                                                                                                                        VYDQEKQVRTMLLSGEPMEFNRVDCLLFVMRDITERRKAEKQLKILSQACEQSPASIVIT
                                                                                                                                                                                                                                                                                                                                               IMDVNQPFCQFFGLTKQELVGVSRQQFYFWVDEQQRQSFLRDLLLWQKDGLVKFENREIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSSLT---VPVMQDQQLWGIMAVHHSKPRRFTEQEWETMALLSKEVSLAITQSQLSRQVHQ
                                                                                                               --QQGIVTHYVAVKEDITKEKQQAEALFHQAHYDHLTGLPNRILAKDRLQQAIESALRQK
                                                                                                                                                                         LASGRNWHGEFHNRRKNGEL--YW----
                                                                                                                                                                                                                                                           -VQS--TWEKPRPFTSVAPLPPTNCVPHGYTLGELEQRSDWIAPPESLSAENFQSFLIVP
                                                                                                                                                                                                                                                                                                                                                                                                        -QTNQALLQKNQQLEEQIEKTARTQAALMQS-----EINFAVAFNQSPDPIFIYGRNSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 QQVQEALVQRLETTVAQYGDRPETWQYALETVGQAVEADGAVLY-IAPD------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteome;
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IPRO01789; Res
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; IPR000160; DUF9.
; IPR001610; PAC.
; IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             840 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGDEF;
PAC; 1.
PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                       ------LTG-SVAQHYQWNLRFDWGNWL-ETSLWQE------
                                                                                                                                                                                                                                                                                                                      LMRGQP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phosphorylation; Sensory transduction 96226 MW; 5F56F3D367B2D9B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%;
28.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 801.5; DB 16; Pred. No. 4.8e-47;
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                                                                                                                                                                                                                                 -GYKSAEVLGRNPRILKSGNKTQEDYE-LMWKT
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                                                                                                                                                                                                                                                                                                                      ----SAAMEPMAA----
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Matches
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Pfam: PF001590; GAF: 1.
Pfam: PF001590; GGDEF: 1.
Pfam: PF00785; PAC: 2.
Pfam: PF00785; PAC: 2.
Pfam: PF00989; PAS: 2.
SMART; SM00267; DUF1: 1.
SMART; SM00065; GAF: 1.
SMART; SM00065; GAF: 1.
SMART; SM00085; PAC: 2.
SMART; SM00091; PAS: 2.
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InterPro;
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                                                                                                                                                                               Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tabuta S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
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GVLSSLTVPVMQDQQLWGIMAVHHSKPRRFTEQEWETMALLSKEVSLAITQSQLSRQVHQ
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                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura T., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IPRO01633; DUF2.
; IPRO00160; DUF9.
; IPRO03018; GAF.
; IPRO01610; PAC.
; IPRO00014; PAS.
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7 (TremBLrel. 02, Last
1 (TremBLrel. 18, Last
AL 178.5 KDA PROTEIN.
                                                                                                                                                                             l protein; Complete
1578 AA; 178546 MW;
                                                                  Conservative
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29.8%;
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                                                                  124;
                                                            Score 797; DB
Pred. No. 2.8e-
24; Mismatches
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; BE1604B60FB456DF CRC64;
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                                                                                       DB 16;
.8e-46;
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Q9L4F1;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                               SEQUENCE FROM N.A.
STRAIN-ATCC 14579 TYPE STRAIN;
MEDLINE=20055637, PubMed=10589720;
Okstad O., Gominet M., Purnelle B., F
"Sequence analysis of three Bacillus
                                                                                                     Bacillus cereus.
Bacteria; Firmicutes; Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID=1396;
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genes encoding degradative enzymes Microbiology 145:3129-3138(1999). EMBL; AJ243712; CAB69812.1; -.

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SMART; SM00091; PAS; 1.
SMART; SM00091; PAS; 1.
SEQUENCE 892 AA; 102
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MLL7787 PROTI
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Rhizobium loti (Mesorhizobium loti)
Bacteria; Proteobacteria; alpha subo
Phyllobacteriaceae; Mesorhizobium.
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MEDLINE=21082930; PubMed=11214968; Raneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamo Kaneko T., Idesawa K., Ishikawa A., Kawashima K., Kimura T Watanabe A., Idesawa K., Kohara M., Matsumoto M., Matsuno A. Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
                                               SEQUENCE FROM N.A. STRAIN=MAFF303099; MEDLINE=21082930;
                                                                              NCBI_TaxID=381;
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Rhizobium loti (Mesorhizobi Plasmid pMLa. Bacteria; Proteobacteria; a Phyllobacteriaceae; Mesorhi NCBI_TaxID=381;

Mesorhizobium

alpha

subdivision;

Rhizobiaceae

group;

(Mesorhizobium loti)

MLR9186 MLR9186

PROTEIN

SEQUENCE

FROM

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Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(2000).
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InterPro; IPR000160; DUF9.
InterPro; IPR000160; PAS.
Pfam; PF00563; EAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF1; 1.
SMART; SM00051; PAS; 2.
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Pfam; PF00563; EAL; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00052; DUF2; 1.
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"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";

DNA Res. 7:331-338(2000).

EMBL; AP003015; BAB54575.1; -.
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LDYLRRVGCDEAQGYLIGKPV
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AP4 related amino
Oat phytochrome A
Synechocystis sp p
Cyanobacterial phy
Synechocystis sp p
                                                                                                                                                                                                                       Description
                                                                                                                                                                                      Mesotaenium
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Arabidopsis thalia	AAG40418	21	315	6.7		5
Arabidopsis thalia	AAG31845	21	290			14
BIV pol gene produ	AAR05614	11	1053		•	ω
Eucalyptus grandis	54	21	990		•	12
s. epidermidis ope	N	22	291		•	H
huma	ABG04356	22	139	6.8	69.5	Ö
Human novel foetal	52	22	97		•	9
	AAB23834	21	2037		•	8
Drosophila	ABB66815	22	555		•	37
Drosophila	ABB65570	22	1366		71	86
S. spin	AAB70969	22	5588		71.5	5
	AAY39301	20	5588		71.5	4
סי	AAU63501	22	500		71.5	ü
Str	AAB13568	21	386		71.5	2
	AAW63721	19	1008	7.0	72	<u>~</u>
Recombinant coll	AAR52579	15	936	7.0	72	ö
	AAY92019	21	407	7.1	•	
	AAY92017	21	407		72.5	
Sequenc	AAP70204	œ	353	•	•	
Tobacco TTG1	AAW97838	20	225		•	9
	AAG91549	22	459		•	5
Arabidopsis TTG1 p	AAW97835	20	341		73.5	24
\mathbf{H}	AAW97836	20	233		•	23
3	ABB65971	22	660		74	22
	AAG43698	21	461		74	21
Arabidopsis thalia	AAG06360	21	461		74	8
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Arabidopsis thalia	AAG06361	21	453		74	8
thal	AAG43700	21	375		74	17
Arabidopsis thalia	AAG06362	21	375	7.2	74	91
rranei	AAW52845	19	4572		4.	5
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a mela	ABB60349	22	1216	8.0		13
Synechocystis sp p	$^{\circ}$	21	950	•		12

ALIGNMENTS

RESULT AAW50145

AAW50145;

AAW50145 standard;

protein;

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ΑĀ

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WPI;
                                                                             02-AUG-1996;
                                                                                                                                                     Mesotaenium caldariorum phytochrome apoprotein.
                                                     Lagarias JC,
                                                                                         01-AUG-1997;
                                                                                                      12-FEB-1998
                                                                                                                  WO9805944-A1.
                                                                                                                              Mesotaenium caldariorum
                                                                                                                                          Phytofluor; fluorescent label; phytochrome; green alga.
                                                                                                                                                                  28-AUG-1998
                                                                 (REGC ) UNIV CALIFORNIA.
                                         1998-145711/13.
                                                                                                                                                                  (first entry)
                                                    Murphy JT;
                                                                              96US-0023217.
                                                                                         97WO-US13529
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Adducts of apoprotein polypeptide and chromophore as label, particularly for bio-molecules - used as fluorescent markers in immunoassays, nucleic acid hybridisation, detecting protein-protein interaction etc., are stable with high molar absorption

Example 2; Page 64; 87pp; English.

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RESULT
AAG62367
ID AAG6
XX AAG6
AC AAG6
AC AAG6
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KW Pher
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Matches 147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises a phytochrome of the green alga Mesotaenium caldariorum. The invention provides a new class of fluorescent protein adducts (phytofluors) that are generally suitable for use as fluorescent markers. They comprise a protein component (an apoprotein) and a bilin chromophore such as phytocerythrobilin. Preferred apoproteins are obtained from plants, e.g. oat (see AAW50144), from green algae, or from cyanobacteria (see algorithms).
                         Bian
                                                                                                                                                                                                                                                                   17-NOV-2000; 2000WO-CN00427
                                                                                                                                                                                                                                                                                                                                                       31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200138515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phenotype switch molecule; gene localisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP4 related amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG62367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG62367 standard;
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                                                                                                    (BIAN/) BIAN X.
                                                                                                                                                                                    19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       383
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||| |||||| ||| ||| ||:||:|| || ||
plrsaceflmqvfglqlnmevelssqlrek 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epylglhypatdipgaarflfmknrvriicdcsappvkviqdptmkhpislagstlrgvh\\
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                        99CN-0121466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein; 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
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Pred. No. 7.2e
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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.2e-85;
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Best Local S
Matches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a method for isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants. The method is useful in gene localisation an classification analysis, studying gene development networks and function networks, and designing drugs based on regulatory sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolating phenotype switch molecules and phenotype-related gene batteries from complex genomes of higher animals and plants, usee.g. in gene localization and classification analysis
                                                                                                                                                                                                                                                                                            Oat phytochrome A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
Adducts of apoprotein polypeptide and chromophore as label particularly for bio-molecules - used as fluorescent marked immunoassays, nucleic acid hybridisation, detecting protein
                                                                                                                                  02-AUG-1996;
                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                                      12-FEB-1998
                                                                                                                                                                                                                WO9805944-A1
                                                                                                                                                                                                                                        Avena sativa
                                                                                                                                                                                                                                                                  Phytofluor; fluorescent label; phytochrome A;
                                                                                                                                                                                                                                                                                                                      28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                       AAW50144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenotypes for disease treatment. The present sequence represents related protein, which is used in an example illustrating the use method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 30-31; 35pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                AAW50144;
                                                                                                                                                                                                                                                                                                                                                                                                                                        380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-367684/38
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                                                                                                       ) UNIV
                                                                              JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                          CALIFORNIA
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                              Murphy JT;
                                                                                                                                 96US-0023217
                                                                                                                                                             97WO-US13529
                                                                                                                                                                                                                                                                                            apoprotein
                                                                                                                                                                                                                                                                                                                                                                       protein; 1129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.1%;
59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 666.5; DB 2
Pred. No. 1.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22;
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                                                                                                                                                                                                                                                                   oat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1128;
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protein-protein markers in

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RESULT AAB26592 ID AAB26592 ID AAB26592 ID AAB26592 ID AAB2 XX AAB2 XX Syne Syne XX Syne XX Syne Syne XX Syne 
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CC Preferred apoproteins are obtained from plants, e.g. oats, from

CC green algae, e.g. Mesotaenium caldariorum (see AAW50145), or from

CC cyanobacteria such as Synechocystis (see AAW50143). Truncated

C apoproteins consisting of the N-terminal chromophore domain are

c especially preferred. Recombinant apoproteins assemble

C comprise a protein, glycoprotein, antibody or nucleic acid to be

C detected linked to the fluorescent adduct. They are used in assays

C comprise a protein glycoprotein, antibody or nucleic acid to be

C detected linked to the fluorescent adduct. They are used in assays

C immunoassay of antigens, immuno-histochemical labelling, as nucleic

C acid probes for Southern blotting, for identification of manufactured

C products, also to detect protein interactions, including

C studies on intracellular protein localisation and identification of

C transfected cells. The phytofluors make ideal fluorescent markers

C because they have a long wavelength absorption maximum and high

C molar absorption coefficient, and are stable to light and pH.
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Best Local
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      19-MAR-1999;
                                                                  14-MAR-2000; 2000WO-US06607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae using a C-terminal epitope tag is provided. The invention provides a new class of fluorescent protein adducts (designated phytofluors) that are generally suitable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interaction
                                                                                                                                                                                                 WO200056355-A1
                                                                                                                                                                                                                                                                                                                          Phytochrome;
                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp phytochrome-related gene Cph1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB26592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB26592 standard; protein; 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 63; 87pp; English
                                                                                                                                  28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises phytochrome A (PHYA) of oat. for the efficient purification of recombinant PHYA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for use as fluorescent markers. They comprise a protein component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPLRYACEFLMQAFGLQLQMELQLASQLAEK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCHTQYMANMGSVASLALAIVVKGKD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 klaakaiskiqslpggsmevlcntvvkevfdltgydrvmaykfheddhgevfseitkpgl 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epylglhypatdipqaarllfmknkvrmicdcrarsikvieaealpfdislcgsalraph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity
126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1129 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etc.,
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                                                                                                                                                                                                                                                                                                                      fluorescent apophytochrome; bilin; Cph
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      99US-0272809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.8%;
59.7%;
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Pred. No. 3e-7
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SSKLWGLVVGHHCSPRYVP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT
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Best Local S
Matches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived from Synechocystis species) and phycoerythrobilin conjugate, useful as fluorescent markers for biological research -
Peptide
                                                                        Peptide
                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                        Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechocystis sp. strain PCC6803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phytofluor; fluorescent label; phytochrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant apoproteins can spontaneously assemble with a variety of bilin chromophore precursors. The present sequence is a phytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 45; 52pp; English.
                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          related protein from Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yhchltylknmgvgasltislikdg----hlwgliachhqtpkvipfelrkacef 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pylglhypesdipqparrlfihnpirvipdvygvavpltpavnpstnravdltesilrsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYLGLHYPATDIPQAARFLFKQNRVRMICDCN--ATPVKVVQSEELKRPLCLVNSTLRAP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-602195/57.
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77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phytochrome Cph1 apoprotein.
                                                                                                                                                                                                                                                                                                           /note= "undetermined amino acid residue"
536..544
                                                                        694..698
                                                                                                                                                      679..687
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709..714
                                                   /note-
                                                                                                                           /note= "histidine
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                                                "histidine
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Pred. No. 2.4e-37;
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motif"
                                                                                                                                                                                                                                                                                  transmitter module
                                                transmitter
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                                                                                                                                                                                                       transmitter module
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyanobacterium
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                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. PCC6803. Its amino acid sequence was deduced from locus slr0473 genomic DNA. Expression of the 748-residue polypeptide in E. coll and incubation with phycocyanobilin yields an adduct with a red, far-red photoreversible phytochrome signature. The invention provides a new class of fluorescent protein adducts (designated phytofluors) that are generally suitable for use as fluorescent markers. They comprise a protein component (an apoprotein) and a bilin chromophore such as phycocrythrobilin. Pareferred apoproteins are obtained from plants, e.g. oats (see AAW50144), from green algae, e.g. Mesotaenlum caldariorum (see apoproteins consisting of the N-terminal chromophore domain are especially preferred. Recombinant apoproteins assemble spontaneously with the bilin chromophore. Claimed compositions
                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                     spontaneously with the bilin chromophore. Claimed compositions comprise a protein, glycoprotein, antibody or nucleic acid to be detected linked to the fluorescent adduct. They are used in assays for detecting the other member of a specific binding pair, e.g. immuno-assay of antigens, immuno-histochemical labeling, as nucleic acid probes for Southern blotting, for identification of manufactured products, also to detect protein-protein interactions, including studies on intracellular protein localisation and identification of transfected cells. The phytofluors make ideal fluorescent markers because they have a long wavelength absorption maximum and high molar absorption coefficient, and are stable to light and pH.
 AAB26600 standard;
                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises cyanobacterial phytochrome 1 (Cph1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adducts of apoprotein polypeptide and chromophore as label, particularly for bio-molecules - used as fluorescent markers in immunoassays, nucleic acid hybridisation, detecting protein interaction etc., are stable with high molar absorption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lagarias JC,
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                                                                                                                                                                                                           manaalnrlrg--ganlrdfydviveevrrmlgfgrvmlyrrdennhcdvialdkrddme 196
                                                                              yhchltylknmgvgasttislikdg----hlwgliachhqtpkvipnelrkaqe
                                                                                                            HGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACE 173
                                                                                                                                           pllqlhypesd1pqparrifihnpirvipdvygvavpltpavnpstnravdltesilrsa
                                                                                                                                                                         PYLGLHYPATDIPQAARFLFKQNRVRMICDCN--ATPVKVVQSEELKRPLCLVNSTLRAP
                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                        Similarity 36.8 64; Conservative
                                                                                                                                                                                                                                                                                                                                                            748
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                                                                                                                                                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                             28.5%;
36.8%;
                                                                                                                                                                                                                                                                              38;
 212
                                                                                                                                                                                                                                                                            Score 292; DB 19;
Pred. No. 8.5e-26;
8; Mismatches 64
 A
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                                                                                                                                                                                                                                                                                                         Length 748;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Fig 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived from Synechocystis species) and phycoerythrobilin conjugate, useful as fluorescent markers for biological research - \,
               Phytochrome;
                                             Synechocystis sp phytochrome-related gene Cph2
                                                                               01-FEB-2001
                                                                                                              AAB26593;
                                                                                                                                              AAB26593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention is related to fluorescent apophytochrome-bilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-602195/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lagarias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synechocystis sp phytochrome-related gene Cph2-N197 peptide
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                                                                                                                                                                                                                              128
                                                                                                                                                                                                                                                             121 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPR 162
                                                                                                                                                                                                                                                                                             71
                                                                                                                                                                                                                                                                                                               64 LGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELK----RPLCLVNSTLRAPH
                                                                                                                                                                                                                                                                                                                                                            20 raltlretl-----qviveeariflgvdrvkiykfasdgsgevlaeavnraalpsl
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                          5 RAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSE-IRRSDLEPY 63
                                                                                                                                                                                                                            schiqyllamgvlssltvpvm----qdqqlwgimavhhskpr
                                                                                                                                                                                                                                                                                        lglhfpvedippqareelgnqrkmiavdvahrrkk---shelsgrisptehsnghyttvd 127
                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JC;
                                                                                                                                            standard; protein; 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
               fluorescent apophytochrome; bilin; Cph
                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          18.6%;
31.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 190; DB 21;
Pred. No. 2.6e-14;
4; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                              165
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212; 20;

Gaps

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41

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RESULT
AAB2657
ID AAB8
XX AAB6
XX AAB6
XX Sync
DT 01-I
DT 01-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 51; Conser
   19-MAR-1999;
                                                           14-MAR-2000; 2000WO-US06607
                                                                                                                                                                                                                                                                                             Phytochrome; fluorescent apophytochrome; bilin; Cph
                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp phytochrome-related gene Cph6
                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB26597 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is related to fluorescent apophytochrome-bilin conjugates, known as phytofluors. An apoprotein known as Cph2 from Synechocystis species is used as the apophytochrome and the bilin is preferably phycocrythrobilin. The phytofluors are useful as fluorescent markers for biological research. The phytofluors have a long wavelength absorption maxima, a high molar absorption coefficient and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived from Synechocystis species) and phycoerythrobilin conjugate, useful as fluorescent markers for biological research -
                                                                                                                      28-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant apoproteins can spontaneously assemble with a variety of bilin chromophore precursors. The present sequence is a phytochrome related protein from Synechocystis sp.
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                                                                                                                                                                                 WO200056355-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71،
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lglhfpvedippqareelgnqrkmiavdvahrrkk---shelsgrisptehsnghyttvd 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELK----RPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     raltlretl-----qviveeariflgvdrvkiykfasdgsgevlaeavnraalpsl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schiqyllamgvlssltvpvm----gdqqlwgimavhhskpr 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1276 AA
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99US-0272809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 844 AA.
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    Matches

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Best Local
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                                                                                                                                                                                 Synechocystis sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived from Synechocystis species) and phycoerythrobilin conjugate, useful as fluorescent markers for biological research -
           Lagarias JC;
                                        (REGC ) UNIV CALIFORNIA.
                                                                                              14-MAR-2000;
                                                                                                                          28-SEP-2000
                                                                                                                                                      WO200056355-A1
                                                                                                                                                                                                              Phytochrome;
                                                                                                                                                                                                                                          Synechocystis sp phytochrome-related gene Cph3
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                                                                   19-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYM 127
                                                                                                                                                                                                                                                                                                                                                                                                  tlyeqaqqelasknqlfvqltneleqk
                                                                                                                                                                                                                                                                                                                                                                                                                               C--EFLMQAFGLQLQMELQLASQLAEK 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         arlqvranlvlpli----ndailwgllcihqcdssrvweqteidllkqitnqfeiaiqqa 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYV-----
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46; Conserv
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                                                                                              2000WO-US06607
                                                                                                                                                                                                              fluorescent apophytochrome; bilin; Cph
                                                                                                                                                                                                                                                                     (first entry)
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Pred. No. 2.2e-05;
9; Mismatches 72
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RESULT 1
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Best Local s
Matches 39
                                                    WPI;
Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived Synechocystis species) and phycoerythrobilin conjugate, useful a fluorescent markers for biological research -
                                                                                                                                                                                                                                                                              Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is related to fluorescent apophytochrome-bilin conjugates, known as phytofluors. An apoprottein known as Cph2 from Synechocystis species is used as the apophytochrome and the bilin is preferably phycoerythrobilin. The phytofluors are useful as fluorescent markers for biological research. The phytofluors have a long wavelength absorption maxima, a high molar absorption coefficient and the
                                                                                                                             19-MAR-1999;
                                                                                                                                                    14-MAR-2000;
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                                                                            Lagarias
                                                                                                                                                                              28-SEP-2000
                                                                                                                                                                                                                             Synechocystis
                                                                                                                                                                                                                                                      Phytochrome;
                                                                                                                                                                                                                                                                                                                              AAB26599,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  recombinant apoproteins can spontaneously assemble with a variety of bilin chromophore precursors. The present sequence is a phytochrome related protein from Synechocystis sp.
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                                                                                                     (REGC
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                                                    2000-602195/57
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                                                                                                   ) UNIV
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                                                                                                     CALIFORNIA
                                                                                                                                                                                                                                                    fluorescent apophytochrome; bilin; Cph
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Pred. No. 4e-0
37; Mismatches
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Best Local S
Matches 49
                                                    Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 (derived from Synechocystis species) and phycoerythrobilin conjugate, useful as fluorescent markers for biological research -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conjugates, known as phytofluors. An apoprotein known as Cph2 from Synechocystis species is used as the apophytochrome and the bilin is preferably phycoerythrobilin. The phytofluors are useful as fluorescent markers for biological research. The phytofluors have a long wavelength absorption maxima, a high molar absorption coefficient and the
                               Example 1;
                                                                                                                   Lagarias
                                                                                                                                                                                                                                                  Synechocystis
                                                                                                                                                                                                                                                                                           Synechocystis sp phytochrome-related
                                                                                                                                                                                                                                                                                                                01-FEB-2001
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                                                                                                                                        (REGC ) UNIV CALIFORNIA
                                                                                                                                                              19-MAR-1999;
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                                                                                                                                                                                                                                                                        Phytochrome;
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                                                                                                                                                                                                                                                                                                                                                                                                               313
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                              Page 47; 52pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                    2000WO-US06607
                                                                                                                                                                                                                                                                     fluorescent apophytochrome; bilin; Cph
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26.5%;
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Pred. No. 0.0001;
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known as phytofluors.

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fluorescent apoprotein

apophytochrome-bilin known as Cph2 from

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conjugates, known as phytofluors. An apoprotein known as Cph2 from Synechocystis species is used as the apophytochrome and the bilin is preferably phycoerythrobilin. The phytofluors are useful as fluorescent markers for biological research. The phytofluors have a long wavelength absorption maxima, a high molar absorption coefficient and the recombinant apoproteins can spontaneously assemble with a variety of
                                                                                                                                      Fluorescent apophytochrome-bilin conjugates, e.g. Cph2 Synechocystis species) and phycoerythrobilin conjugate, fluorescent markers for biological research -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinant apoproteins can spontaneously assemble bilin chromophore precursors. The present sequence related protein from Synechocystis sp.
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                                                                   The present invention is related to fluorescent apophytochrome-bilin conjugates, known as phytofluors. An apoprotein known as Cph2 from
                                                                                                                                                                                                WPI; 2000-602195/57
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                                                                                                               Example 1;
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                                                                                                                                                                   (derived
                                                                                                                                                      useful
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                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
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                                                                                                           Disclosure;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                       pharmaceutical.
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                      identification of prodomain regions located N-terminal to the mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the climical condt. or reproductive physiology of
                                                                                                                                                                                                   Recombinant human or modulating clinical c
                                                                                                 A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the
                                                                                                                                                                Claim 30(b); p 22; 48pp; English
                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                     Mason
                                                                                                                                                                                                                                                                                                                     10-FEB-1986;
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03-OCT-1985;
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at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC
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nes 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ececglvwfghwlrrwlresaqikviqkddlkr-----mvqsp--cqhlprsnigstp 1143
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85US-0783910
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RESULT 1
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                      The present sequence represents a Amycolatopsis mediterranei rifamycin CC synthesis gene cluster ORF A protein from the present invention. The CDNA fragment comprises a DNA region involved directly or indirectly continuously in the gene cluster responsible for rifamycin synthesis, including CC the adjacent DNA regions to the right and left which, by reason of their function in connection with rifamycin biosynthesis, qualify CC as constituents of this rifamycin gene cluster, and functional CC mediterranei rifamycin synthesis gene cluster, and functional CC mediterranei rifamycin synthesis gene cluster DNA fragment can be used CC be used for inactivating or modifying genes involved in ansamycin or CC rifamycin biosynthesis. The DNA can be used for constructing mutant CC constructs strains from which the natural rifamycin or ansamycin CC biosynthesis gene cluster has been partly or completely deleted. The CC DNA fragment can be used for assembling a library of polyketides. CC A hybridisation probe of the invention can be used for identifying DNA CC fragments involved in the biosynthesis of ansamycins.
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Best Local
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                                                                                                                                                                                                                                                                                                                              Amycolatopsis mediterranei rifamycin synthesis to produce rifamycin and rifamycin analogues
                                                                                                                                                                                                                                                                                                                                                                                                                  Engel N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1996;
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Search completed: June 7, 2002, 18:55:15 Job time: 269 sec
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                                                          3025 ds-----peelwklvaegrdavsgfpvdrgwdldglyhpdpahagtsytrsggflh 3075
                                                                          170 YACEFLMQAFGLQLQMELQLASQ 192
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Result
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

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Copyright (c) 1993 - 2000 Compugen
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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US-08-904-871-15
US-08-904-871-13
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RESULT 1 US-08-904-87 Sequence 4 Patent No. GENERAL IN APPLICANT TITLE OF FILE REFE. CURRENT A C	00000000000000000000000000000000000000
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871-4 4, Applicatio 6, 6046014 INFORMATION: NT: LAGRATION: NT: LAGRATION: NT: LAGRATION: PERENCE: 2500 FINVENTION: FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION FILING DATE: APPLICATION: APPLICATION: APPLICATION: INFORMATION: BATTIFICIAL E: INFORMATION: AND INFORMAT	$\begin{array}{cccccccccccccccccccccccccccccccccccc$
ion US/08904 , John C John T PHYTOFLUORS 0.134UORS 0.134UORS 0.197-08-01 NUMBER: G0/ 1997-08-02 S: 16 Ver. 2.0 Ver. 2.0 Ver. 2.0 Ver. 2.0 LPGGDIGALCDT LPGGDIGALCDT LPGGDIGLCDA LPGGDIGLLCDA LPGGDIGLLCDA LPGGDIGLLCDA LPGGARFLENGN 11111111111111111111111111111111111	414 1178 413 206 313 399 399 399 399 313 2548 1151 1151 1151 1151 1151 323 323 323 394
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1 S FLUGRESCENT LA TT LAGARIAS PATE 7904,871 3,217 3,217 3,217 3,217 3,217 Seq. No. 1.4e-90; Mismatches 29 EDVORLTGYDRVMYVO [: : [: : EEVRELTGYDRVMYVVOS ENTRELTGYDRVMYVVVOS [: :	US-09-270-751-2 US-09-147-928-4 US-09-147-928-2 US-09-311-311C-22 US-09-347-803-25 US-08-989-386-1 US-08-750-134A-5 US-08-363-757-2 US-09-172-422-1 US-08-332-576-3 PCT-US95-13672-3 US-08-521-872-18 US-08-521-872-18 US-08-521-872-18 US-08-551-868B-17 ALIGNMENTS
BELS nt uence:: Sequence Length 611; Indels 14; Gaps 1 FHEDDHGEVVSEIRRSDL 60 [: :: : FHEDEHGEVIAEIRRSDL 262 EELKRPLCLVNSTLRAPH 120 :	Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 22, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 18, Appli

RESULT 2 US-08-904-871-12 ; Sequence 12, Application US/08904871 ; Patent No. 6046014

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                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 554
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APPLICANT: Lagarias, John C
APPLICANT: Mirphy, John T
ITTLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134050 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER APPLICATION NUMBER: 60/023,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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SEQ ID NO 12
LENGTH: 1142
TYPE: PRT
                                                                                                                                  Matches 145;
                                                                                                                                                                       Query Match
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APPLICANT: Murphy, John T
APPLICANT: Murphy, John T
TITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILLING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILLING DATE: 1996-08-02
NUMBER OF SEO ID NOS: 16
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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      61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                      Local Similarity
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                                                                     1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
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                                               KLAAKAISRLQSLPGG-MELLCDTVVEEVRELTGYDRVMAYKFHEDEHGEVVAEI-RPDL 238
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                                                                                                                                  Conservative
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                                                                                                                                  20;
                                                                                                                                                    Score 733; DB 3; Pred. No. 4.8e-84;
                                                                                                                                  Mismatches
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APPLICANT: MUPPHY, John T
TITLE OF INVENTION: PHYTOFIUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.1344G9 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 600
APPLICANT: Lagarias, John C
APPLICANT: Murphy, John T
ITTLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.1134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1966-08-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                       Sequence 2, Application US/08904871 Patent No. 6046014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPYLGLHYPATDIPQAARFLFMKNKVRMIVDCNAKHARVLQDEKLSFDLTLCGSTLRAPH
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; TYPE: PRT
; ORGANISM: Oat (Avena)
US-08-904-871-11
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US-08-904-871-11
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LENGTH: 600
TYPE: PRT
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APPLICANT: Lagarias, John C
APPLICANT: Murphy, John T
TITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 11
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Best Local Similarity
Matches 126; Conserv
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                                                                                                                                                                                                                                                                                            y Match 64.8%; Score 663.5; DB 3; Local Similarity 59.7%; Pred. No. 9.1e-75; hes 126; Conservative 24; Mismatches 46;
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                                                                                                       GCHTQYMANMGSVASLALAIVVKGKD------SSKLWGLVVGHHCSPRYVP 165
                                                                                                                                                               EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
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FPLRYACEFLAQVFAVHVNREFELEKQLREK 411
                                                                   SCHLQYMENMNSIASLVMAVVVNENEEDDEAESEQPAQQQKKKKLWGLLVCHHESPRYVP
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                                  FPLRYACEFLMQAFGLQLQMELQLASQLAEK 196
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59.7%;
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; Pred. No. 3.4e-75;
24; Mismatches 46;
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                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial US-08-904-871-6
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                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver.
SEQ ID NO 6
LENGTH: 748
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Best Local Similarity 44.0
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SEQ ID NO 5
LENGTH: 528
                                                                Query Match
Best Local Similarity
Matches 77; Conserv
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APPLICANT: MUIPDY, JOHN T
TITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Murphy, John T
APPLICANT: Murphy, John T
ITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEO ID NOS: 16
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                                                                                                                                                                                                                       FEATURE:
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PYLGLHYPESDIPQPARRLFIHNPIRVIPDVYGVAVPLTPAVNPSTNRAVDLTESILRSA
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                                                                    Conservative
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                                                                37.9%; Score 388; DB 3; I
44.0%; Pred. No. 3.8e-40;
"". wismatches 53;
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Pred. No. 2.2e-40;
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RESULT 9
US-08-904-871-13
; Sequence 13, Application US/08904871

    patent No. 6046014
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US-08-904-871-13
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GENERAL INFORMATION:
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Best Local 9
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APPLICANT: Murphy, John T
APPLICANT: Murphy, John T
ITLE OF INVENTION: PHYTOFLUORS AS FLUORESCENT LABELS
FILE REFERENCE: 2500.134US0 UC OTT Lagarias Patent
CURRENT APPLICATION NUMBER: US/08/904,871
CURRENT FILING DATE: 1997-08-01
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER APPLICATION NUMBER: 60/023,217
EARLIER FILING DATE: 1996-08-02
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
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                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    APPLICANT: Anthony J. Mason
APPLICANT: Peter H. Seeburg
TITLE OF INVENTION: NUCLEIC
NUMBER OF SEQUENCES: 44
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                                                                                                   COUNTRY:
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nes 77; Conserv
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Pred. No. 3.8e-40;
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US-08-459-850-43
; Sequence 43, Application US/08459850
; Patent No. 5665568
; GENERAL INFORMATION:
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Best Local Similarity 34.4%;
                                                                                                                                                                       APPLICANT: Anthony J. Mason APPLICANT: Peter H. Seeburg TITLE OF INVENTION: Nucleic A TITLE OF INVENTION: Beta Chai TITLE OF INVENTION: Using suc NUMBER OF SECUENCES: 44
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ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
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FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
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LENGTH: 353 amino acid
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ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 29
SLECOMMUNICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 NA-----TPVKVVQSEELKRPLCLVNSTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRWICD--C 92
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                      STREET:
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FILING DATE: 12-AUG-1991
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                                                                                 COUNTRY:
                                                                                                                                                          ADDRESSEE:
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South San Francisco
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                                                                                                California
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Beta Chains of Inhibin and Method
Using such Nucleic Acid
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Bruno
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Pred. No. 1.1;
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SOFTWARE: patin (Genen CURRENT APPLICATION DATA:

OPERATING SYSTEM:

PC-DOS/MS-DOS

US/08/459,850

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                                                                                                                                                                                                           Sequence 43, Application US/08459214 Patent No. 5716810 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.18;
Best Local Similarity 34.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                       APPLICANT: Anthony J. Mason APPLICANT: Peter H. Seeburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 06/906729
FILING DATE: 31-DEC-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/827710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 07/215466
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                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                     199 DSCQELAVVPVFVDPGEESHRPFVVVQARL 228
                                                                                                                                                                                                                                                                                                                                                                                                          144 RVKYY-FQEQGHGDRWNMYEKRVDLK-RSGWHTFPLTEAIQA---LFERGERRLNLDVQC 198
             CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                       93 NA-----TPVKVVQSEELKRPLCLVNSTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                 37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRMICD--C 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/9: FILING DATE: 08-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/19
FILING DATE: 17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                   DDRESSEE:
                                              E: Genentech, Inc.
460 Point San Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-1988
                                                                                                                 Nucleic Acid Encoding the Alpha or
Beta Chains of Inhibin and Method for Synthesizing Polypeptide
Using such Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07/744207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 72.5; DB Pred. No. 1.1; 14; Mismatches
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PCT-US93-05944-2

Sequence 2, Application PC/TUS9305944 GENERAL INFORMATION:

APPLICANT: Lin et al., Hun-Chi TITLE OF INVENTION: Molecular of TITLE OF INVENTION: responsible

Molecular cloning of the genes responsible for collagenase pr

collagenase product

CORRESPONDENCE ADDRESS:
ADDRESSEE: Harris Brotman
STREET: 401 B. St Ste 1700

San Diego : CA

NUMBER OF SEQUENCES:

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                                                                                                                                      Query Match
Best Local Similarity
Matches 31; Conserv
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 06/71
FILING DATE: 03-OCT-1985
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER: 08/1:
FILING DATE: 17-FEB-1994
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199 DSCQELAVVPVFVDPGEESHRPFVVVQARL 228
                                                                   144 RVKVY-FQEQGHGDRWNMVEKRVDLK-RSGWHTFPLTEAIQA---LFERGERRLNLDVQC 198
                                                                                       37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRMICD--C 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 31-DE
                                  93 NA-----TPVKVVQSEELKRPLCLVNSTL 116
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hasak, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 06/8: FILING DATE: 07-FEB-1986
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                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                              : 353 amino acids amino acid
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TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
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12-AUG-1991
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                                                                                                                                                          34.4%;
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                                                                                                                                        14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        297P2D6
                                                                                                                                                      Score 72.5; DB 1;
Pred. No. 1.1;
                                                                                                                                        30;
                                                                                                                                        Indels
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COUNTRY: USA ZIP: 92101-4297

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RESULT 14
US-09-036-987A-6
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 699-3630
TELEPA: (619) 236-1048
FORMATION:
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                                                                                                                                                                                                                                                                                                                      APPLICANT: Treadway, APPLICANT: Turner, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US/0 FILING DATE: 09-MAR-1998
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                   ADDRESSEE:
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AMINO ACID
                                                                                                                                              46268
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                                                                                                                                                                                                                   9330 Zionsville Road
                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                           Treadway, Patti J.
                                                                                                                                                                                                                                                                                                                                                                            Merlo, Donald J.
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Crawford, Kathryn P.
                                                                                                                                                                                                                                                                                                                                                                                               Madduri, Krishnamurthy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baltz, Richard H.
                                                                                                                                                                                                                                   Dow AgroSciences LLC Patent Department
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) 236-1048
T NO: 2:
                                                                                                                                                                                                                                                                                      Production
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              US/09/036,987A
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                                                                                                                                                                                                                                           ; LENGTH: 5588
TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-6
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APPLICANT: Broughton, Mary C
APPLICANT: Broughton, Mary C
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
TITLE OF INVENTION. Biosynthetic Genes For Sp.
FILE REFERENCE: 50489 DIV1
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: US 09/36987
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                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1998-03-09 NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver.
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TELEPHONE: (317)337-4816
TELEFAX: (317)337-4847
                                                                      3445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3547 TTTRAP------VAEDDLVAIVGMGCRFPGQVSSPEELWRLVAG 3584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3445 IRRNRRASGTELADEGTLLGVVREHAAAVLGYSSAADVGVERAFRDLGFDSLSGVELRNR 3504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
3505 LAGVLGVRLPATAVFDYPTPRALARFLHQE----LADEIATTPAPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3505 LAGVLGVRLPATAVFDYPTPRALARFLHQE----LADEIATTPAPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Stuart, Donald R REGISTRATION NUMBER: 28,479 REFERENCE/DOCKET NUMBER: 50
                             60 LEPYLGLHYPATDI-----PQA-ARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 LEPYLGLHYPATDI-----PQA-ARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDR----VMVYQFHEDDHGEVVSEIR-RSD 59
                                                                                                       4 VRAISKLQSLPGGDIGALCDTVVEDVQRLTGYDR---VMVYQFHEDDHGEVVSEIR-RSD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLRAPHGCHTQYMANMGSVASLALAIVVKGKDSS--KLWGLVVG
                                                                      IRRNRRASGTELADEGTLLGVVREHAAAVLGYSSAADVGVERAFRDLGFDSLSGVELRNR 3504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                    5588
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26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 71.5;
Pred. No. 16
                                                                                                                                                 Pred. No. le+(
); Mismatches
                                                                                                                                                                                    Score 71.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1e+02;
                                                                                                                                                                    1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spinosyn Insecticide
                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 5588;
                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                    Length 5588;
                                                                                                                                                 Indels
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                                                                                                                                                 Gaps
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OM protein -
protein search, using sw model
                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Run June 7, 2002, 18:56:32; Search time 37.51 Seconds (without alignments) 502.093 Million cell updates/sec

Perfect score: US-09-272-809-9 1024

Sequence: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum Maximum DB DB seq seq length: 0 length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries Maximum Match 100%

Database PIR_71:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	σ	5	4	ω	2.	1	Result No.
666.5	668	668.5	669.5	671.5	672	672	687	706	707	717.5	723.5	734.5	740.5	746	747	763.5	763.5	•	772	783	785	794.5	802.5	806	828	836	840.5	1024	Score
65.1	ū			65.6	5	5	7.	68.9	69.0	70.1	70.7	71.7	72.3	72.9	72.9	74.6	74.6	74.8	<u>ب</u>			77.6	78.4	78.7		81.6	82.1	100.0	Query Match
1129	1129	495	1129	1123	1122	1122	1465	1111	210	211	1303	1135	1132	368	1134	1129	577	1136	1156	1164	1142	1171	1172	1039	1132	1135	1131	1112	Length
2	N	2	N	Ŋ	N	_	Ŋ	-	N	N	۳	N	N	N	2	N	2	N	N	2	2	N	٢	N	N	N	N	Ŋ	DB
S00097	S52631	800098	A29631	S20497	D86229	FKMUA	T30891	FKMUC	S62721	S62720	S27396	T14803	S37206	T09496	S31280	S28431	S58130	T14842	T07756	B71429	S62714	S14065	FKMUB	T14802	T03668	т16973	T09701	S46313	ID
4 -	Α.	5	w '	A	A [i	Α.	: :		в2 -	В	rd /	C	•	•	· Ma	phytochrome B - po	,	- NC	₩.		1ь -	Β.	H	В.	8	B	- Sc	ochrome E -	Description

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LQLQMELQLASQLAEK 196

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381 181 321 121 261

LQLQMELQLASQLAEK

396

Ωy В

GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 180

Qy

61

Qy

1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 260

EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATFVKVVQSEELKRPLCLVNSTLRAPH 120 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH

320

Matches 196;

Best

y Match 100.0%; Local Similarity 100.0%; hes 196; Conservative 0

0;

Score 1024; DB 2; Pred. No. 1.8e-92; Mismatches 0;

Indels Length 1112;

0;

Gaps

0;

밁

201

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665.5 65.0 1124 1 FKPUZ 665.5 65.0 1124 2 SO68956 665.5 65.0 1128 2 SO3728 phytochrome 665.5 65.0 1128 2 SO3728 662.5 64.7 1125 2 TO9835 660.5 64.7 1125 2 TO9835 660.5 64.7 1121 2 TO7137 660.6 63.1 1131 2 TO7137 584.5 57.1 190 2 S46926 584.5 57.1 190 2 S46926 584.5 57.1 190 2 S46927 584.5 156 2 S46927 584.5 156 2 S46928 585.5 149.6 156 2 T14838 587.5 49.6 314 2 T14839 587.5 49.6 315 2 T14836 587.5 44.5 115 2 T09337 587.5 phytochrome 588.6 156 2 T14836 588.7 1 156 2 T14836 589.7 1 156 2 T17026	45	44	43	42	41	40	39	38	37	36	35	34	33	32	3 11	30
1124 1 FKPUZ phytochrome 1124 2 S06856 phytochrome 1128 2 S03728 phytochrome 1128 2 T09835 phytochrome 1121 2 T09835 phytochrome 1131 2 T07137 phytochrome 1131 2 T07137 phytochrome 1131 2 T07137 phytochrome 1130 2 S46926 phytochrome 14837 phytochrome 14837 phytochrome 14848 phytochrome 14848 phytochrome 14848 phytochrome 1584 2 T14838 phytochrome 1585 2 T14836 phytochrome 1586 2 T14836 phytochrome 1586 2 T14839 phytochrome 1587 2 T19337 phytochrome 1588 phytochrome 1589 phytochrome 1589 phytochrome 1589 phytochrome 1589 phytochrome 1589 phytochrome	455.5	474	489	501	507.5	513	521	548	561	584.5	646	660.5	662.5	665.5	665.5	666
1 FKPUZ phytochrome 2 \$06856 phytochrome 2 \$03728 phytochrome 2 \$03728 phytochrome 2 \$109835 phytochrome 2 \$109835 phytochrome 2 \$107137 phytochrome 2 \$146926 phytochrome 2 \$146927 phytochrome 2 \$146928 phytochrome 2 \$146928 phytochrome 2 \$14636 phytochrome 2 \$114838 phytochrome 2 \$114839 phytochrome 2 \$114839 phytochrome 3 \$114839 phytochrome 4 \$114839 phytochrome 5 \$114830 phytochrome 5 \$114830 phytochrome 6 \$1709337 phytochrome	44.5	46.3	47.8	48.9	49.6	50.1	50.9	53.5	54.8	57.1	63.1	64.5	64.7	65.0	65.0	65.0
phytochrome	115	105	156	156	314	156	197	189	156	190	1131	1131	1125	1128	1124	1124
phytochrome	Ν	N	N	N	N	N	N	N	N	N	Ν	N	N	N	N	μ
	T09337	T17026	T14836	T14839	T14865	T14838	S46928	S46927	T14837	S46926	T07137	JQ0382	T09835	S03728	S06856	FKPUZ
- zucc - gard (close A - Po A - ma A - ma A - so A - so A - so C - Nymp - Char - Norw 4 - Norw 4 - Norw 5 - Pour																
	Ø	O	æ	phytochrome 4 -	w	phytochrome 3 -	phytochrome - C	æ	ര	æ	phytochrome A -	phytochrome A -	phytochrome A -		phytochrome - gard	phytochrome - zuco

ALIGNMENTS

A:Map position: 4
A:Introns: 665/1; 934/2; 1032/2
A:Introns: 665/1; 934/2; 1032/2
C:Superfamily: phytochrome; phytochrome homology
C:Keywords: chromoprotein; photoreceptor; phytochromobilin
E:63-569/Domain: phytochrome homology <PHYT>
F:322/Binding site: phytochromobilin (Cys) (covalent) #stat phytochrome E - Arabidopsis thaliana N;Alternate names: protein F1555.100 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 05-May-2000 C;Accession: S46313; T14813; S41912 R;Clack, T; Mathews, S; Sharrock, R.A. Plant Mol. Biol. 25 413-427, 1994 A;Title: The phytochrome apoprotein family in Arabidopsis is encoded by five A;Reference number: S46312; MUID:94325466 A;Accession: S46312; MUID:94325466 A; Molecule type: DNA
A; Residues: 1-1112 <BEV>
A; Cross-references: EMBL: AL110123; GSPDB: GN00062; ATSP: F15J5.100
A; Experimental source: Cultivar Columbia; BAC clone F15J5
C; Genetics: A;Cross-references: EMBL:X76610; NID:g452815; PIDN:CAA54075.1; R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; submitted to the Protein Sequence Database, August 1999 A; Gene: phyE; ATSP:F15J5.100 A; Reference number: Z18120 A; Accession: T14813 A; Molecule type: DNA A; Residues: 1-1112 <CLA> (Cys) (covalent) #status predicted PID:g452817 Mewes, H.W.; Mayer, genes:

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phytochrome - Scotch pine
C;Species: Pinus sylvestris (Scotch pine)
C;Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C;Accession: T09701
R;Wiegmann-Eirund, C.M.; Kolukisaoglu, H.U.
submitted to the EMBL Data Library, March 1996
A;Reference number: 216826
A;Accession: T09701
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1131 <WIE>
A;Cross-references: EMBL:X96738; NID:g1237083
A;Experimental source: isolate PsA 5.1
C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;75-587/Domain: phytochrome homology <PHY>
F;332/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                       A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1135 < HUD>
A; Cross - references: EMBL:Y14676; NID:g2370330; PIDN:CAA74992.1;
A; Cross - references: cultivar PBHID; leaf
C; Genetics:
A; Gene: PHYB
C; Gene: PHYB
C; Superfamily: phytochrome; phytochrome homology
C; Keywords: chromoprotein; photoreceptor; phytochromobilin
F; 82-592/Domain: phytochrome homology <PHY>
F; 338/Binding site: phytochromobilin (Cys) (covalent) #status pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                       phytochrome B - curled-leaved tobacco
C;Species: Nicotiana plumbaginifolia (curled-leaved tobacco)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T16973
R;Hudson, M.E.; Robson, P.R.H.; Kraepiel, Y.; Caboche, M.; Smith, H.
Plant J. 12, 1091-2101, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
T16973
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                                                                                                                                                                                                                                                                                                                                                                                          Plant J. 12, 1091-2101, 1997
A;Title: Nicotiana plumbaginifolia hlg mutants
A;Reference number: 218626; MUID:98079245
A;Accession: T16973
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1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCHTQYMANMGSVASLALAIVVKGKD-----SSKLWGLVVGHHCSPRYVPFPLRYA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEFLMQALGLQLNMELQLAAQLTEK 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCHAQYMANMGSIRSLLMAVIINGNDDEGGGSGRNSMKLWGLVVCHHTSPRAVPFPLRYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLAVRAISRLQSLPCGDVGLLCDTVVENVRELTGYDRVMVYKFHEDEHGEVVAEIRRSDL
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                                                                 Similarity
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                 81.6%;
77.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.1%;
78.0%;
                                             18;
                                                               Score
Pred.
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Pred. No. 2.
                                             Mismatches
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                                                                 836;
No. 6.
                                                                 DB 2;
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                                                                                 Length 1135;
                                             Indels
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RESULT 5 T14802 phytochrome

B

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sorghum

(fragment)

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A;Accession: T03668
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1132 <KER>
A;Residues: 1-1132 <KER>
A;Residues: 1-1132 <KER>
A;Cross-references: EMBL:L1.0114; NID:g295345; PIDN:AAA34092.1; PID:g295346
A;Experimental source: strain SR1; tissue-type etiolated seedling
R;Lopez-Juez, E; Nagatani, A.; Tomizawa, K.; Deak, M.; Kern, R.; Kendrick, R.E.; Fur Plant Cell 4, 241-251, 1992
Plant Cell 4, 241-251, 1992
A;Title: The cucumber long hypocotyl mutant lacks a light-stable PHYB-like phytochrom A;Reference number: Z14997; MUID:92361250
A;Accession: T03672
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: phytochrome; phytochrome homology C;Keywords: chromoprotein; photoreceptor; phytochromobilin F;80-589/Domain: phytochrome homology <PHY> F;336/Binding site: phytochromobilin (Cys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 457-506, 'S', 508-586, 'Q', 587-1132 < LOP>
A; Cross-references: EMBL: M65023; NID: g170286; PIDN: AAA34093.1;
C; Genetics:
A; Gene: phyB
C; Superfamily: phytochrome; phytochrome homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phytochrome B - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar
C;Accession: T03668; T03672
R;Kern, R.; Gasch, A.; Deak, M.; Kay, S.A.; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: PhyB of tobacco, a new member of the photoreceptor A; Reference number: Z14996; MUID:94105358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
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Best Local S
Matches 156
  395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.; Gasch, A.; Deak, M.; Kay, S.A.; Chua, N.H.
hysiol. 102, 1363-1364, 1993
                                                                                                                                                                                                                                                                     1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                     EFLMQAFGLQLQMELQLASQLAEK 196
                                                                                                       GCHTQYMANMGSVASLALAIVVKGKD------SKLWGLVVGHHCSPRYVPFPLRYAC
                                                                                                                                                                                     EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                  KLAVRAISHLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKIPDL
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EFLMQAFGLQLNMELQLASQLSEK
                                                                               GCHAQYMANMGSIASLTLAVIINGNDEEAVGGRSSMRLWGLVVGHHTSARCIPFPLRYAC
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                                                                                                                                                                                                                                                                                                                                  156;
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                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                     80.9%;
76.5%;
                                                                                                                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                             Score 828; DB Pred. No. 3.8e 18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                     DB 2;
.8e-73;
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A; Molecule type: DNA
A; Residues: 1-1039 <CHI>A; Residues: 1-1039 <CHI>A; Cross-references: EMBL-U56730; NID:g1800216; PID:g1800217
A; Experimental source: cultivar 58M
C; Genetics:
A; Gene: PHYB
A; Note: Intron positions not resolved (incomplete sequence)
C; Superfamily: phytochrome, phytochrome homology
C; Keywords: chromoprotein; photoreceptor; phytochromobilin
F; 233/Binding site: phytochromobilin (Cys) (covalent) #status
Nature 402, 761-768, 1999
A;Title: Sequence and analys
A;Reference number: A84420;
A;Accession: F84568
A;Status: preliminary
                                                                                            A;Molecule type: DNA
A;Residues: 1-1172 <REE>
A;Cross-references: GB:L09262
A;Experimental source: ecotype Landsberg, mutant hy3
A;Experimental source: ecotype Landsberg, mutant hy3
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-1172 <SHA>
A; Residues: 1-1172 <SHA>
A; Cross-references: EMBL: X17342; NID: 916422; PIDN: C.
R; Reed, J.W.; Nagpal, P.; Poole, D.S.; Furuya, M.; Plant Cell 5, 147-157, 1993
Plant Cell 5, 147-157, 1993
A; Title: Mutations in the gene for the red/far-red A; Reference number: JQ2141; MUID: 93200802
A; A; Crossion: JQ2141; MUID: 93200802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: The Sorghum bicolor phot
A;Reference number: Z18185
A;Accession: T14802
A;Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Sharrock, R.A.; Quail, P.H. Genes Dev. 3, 1745-1757, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phytochrome B - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991
C;Accession: B33473; JQ2141; F84588; S07718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Novel phytochrome sequences in Arabidopsis A;Reference number: A3473; MUID:90108670 A;Accession: B33473
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Best Local
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                                                                Sequence and analysis of chromosome
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73.6%;
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Library, April 1996
bicolor photoperiod sensitivity go
                                            MUID:20083487
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Pred. No. 5.1e
21; Mismatches
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5.1e-71;
nes 22;
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                                                              the
                                                                                                                                                                                                                                                                                                           light receptor phytochrome
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                                                                                                                                                                                                                                                                                                                                                                                PID: g16423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                structure,
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A; Molecule type: DNA
A; Residues: 1-1172 <STO>
A; Cross-references: GB: AE002093; NID: g4185145; PIDN
A; Cross-references: GB: AE002093; NID: g4185145; PIDN
C; Genetics:
A; Gene: phyB; At2g18790
A; Map position: 2
A; Introns: 722/1; 991/2; 1088/2
A; Introns: 722/1; 991/2; 1088/2
C; Superfamily: phytochrome; phytochrome homology
C; Keywords: chromoprotein; dimer; photoreceptor; ph; F; 01-614/Domain: phytochrome homology <PHYT>
F; 901-1172/Domain: signal transduction <STD>
                                                                                                                                                                                                                                                                                       C:Superfamily: phytochrome; phytochrome homology C:Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription F:103-623/Domain: phytochrome homology <PHYT> F:364/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phytochrome B - rice
C;Species: Oryza sativa (rice)
C;Date: 19-Mar-1997 #sequence_revision
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A;Residues: 1-1171 <DEH>
A;Cross-references: GB:X57563; NID:g6469490; PIDN:CAA40795.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R; Dehesh, K: Tepperman, J: Christensen, Mol. Gen. Genet. 225, 305-313, 1931 A;Title: phyB is evolutionarily conserved A;Reference number: S14065; MUID:91172131
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F;357/Binding site: phytochromobilin (Cys) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status:
                                                                                                                                                                                                        Query Match
Best Local S
Matches 150
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                                 121
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                                                                                                                                    1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                                                                                                                                                                                                                                                                                                                                                              phyB
                                                                 GCHGQYMANMGSIASLVMAVIISSGGDDDHNIARGSIPSAMKLWGLVVCHHTSPRCIPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YACEFLMQAFGLQLQMELQLASQLAEK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCHTQYMANMGSVASLALAIVV------KGKDSSKLWGLVVGHHCSPRYVPFPLR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                 GCHTQYMANMGSVASLALAIVVK - - GKD - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YACEFLMQAFGLQLNMELQLALQMSEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151;
                                                                                                                                                                                                        al Similarity
150; Conserv
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                        77.6%;
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                                                                                                                                                                                                        Score 794.5;
Pred. No. 7.9e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
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1. No. 1.3e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.H.; Quail,
                                                                                                                                                                                                        1.9e-70;
nes 23;
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                                                                                                                                                                                                                                         DB 2;
                                 SSKLWGLVVGHHCSPRYVPFP 167
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                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                        Length 1171;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71429; S46312; S41910
C;Accession: B71429; S46312; S46312; S41910
C;Accession: B71429; S41910
C;Accession: B71429; S41910
C;Accession: B71429; S41910
C;Access
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A; Residues: 1-1142 <LAG>
A; Residues: 1-1142 <LAG>
A; Residues: 1-1142 <LAG>
A; Cross-references: EMBL; U31284; NID:g1125698; PIDN:AAC49128.1; PID:g1125699
A; Cross-references: EMBL; U31284; NID:g1125698; PIDN:AAC49128.1; PID:g1125699
C; Genetics:
A; Introns: 125/1; 298/3; 393/3; 468/3; 543/2; 621/3; 699/1; 785/1; 856/3; 970/2; 1067/2
C; Superfamily: phytochrome homology
C; Keywords: chromoprotein; photocreceptor; phytochromobilin; transcription regulation
F; 88-589/Domain: phytochrome homology <CHYT>
F; 880-1139/Domain: signal transduction #status predicted <STD>
F; 880-1139/Domain: signal transduction #status predicted <STD>
F; 324/Binding site: phytochromobilin (Cys) (covalent) #status predicted
A; Molecule type: DNA
A; Residues: 1-1164 <BEV>
A; Cross-references: GB:297340; NID:g2244950;
R; Clack, T.; Mathews, S.; Sharrock, R.A.
Plant Mol. Biol. 25, 413-427, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phytochrome D - Arabidopsis thaliana C; Species: Arabidoneio + holina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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A;Title: Atypical phytochrome gene structual, Reference number: 562713; MUID:96191280
A;Accession: S62714
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C;Species: Mesotaenium caldariorum
C;Species: Mesotaenium caldariorum
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-Jun-1999
C;Accession: S62714
                                                                                                                                                                      A; Status: preliminary; nucleic
                                                                                                                                                                                                           A; Reference number: A71400; A; Accession: B71429
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                                                                                                                                                                                                                                             of contiguous MUID:98121113
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                                                                                                                                                                          sequence not shown; translation
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                                                                                                                                                                                                                                                                          sequence
                                                                  PIDN:CAB10404.1;
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                                                                  PID: g2244983
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Rechman, S.; Ans
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64 LGLHYPATDIPQAARELEKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCH 123

IGLHYPATDIPQASRFLFKQNRVRMIVDCHASAVRVVQDEALVQPLCLVGSTLGAPHGCH

4 VRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLEPY 63

Conservative

20;

27;

Indels

8;

Gaps

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VRAISQLQSLPSADVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVSESKRPDLEPY

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A;Gene: phyB
A;Introns: 712/1; 810/3; 987/2; 1085/2
A;Introns: 712/1; 810/3; 987/2; 1085/2
C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin
F;82-612/Domain: phytochrome homology <PHY>
F;358/Binding site: phytochromobilin (Cys) (covalent) #state
                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1156 <HAH>
A;Cross-references: EMBL:L34843; NID:g516102; PIDN:AAA34000.1;
A;Experimental source: strain Paldal; leaf seedling
                                                                                                                                                                                                                                                                                                                                                                                                                                                               phytochrome B - soybean
C;Species: Glycine max (soybean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999
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A,Gene: PHYD
A;Gene: PHYD
A;Map position: 4COp9-4G3845
C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin; transcriptic
F;103-618/Domain: phytochrome homology <PHYT>
F;360/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: T07756
                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A;Description: Nucleotide sequence c
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A;Molecule type: DNA
A;Molecule: 1-424,'F',426-1164 <CLA>
A;Cross-references: EMBL:X76609; NID:g452812; PIDN:CAA54072.1;
C;Genetics:
                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated
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Best Local S
Matches 148
                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.5%; Score 783; DB 2; ilarity 71.2%; Pred. No. 1.1e-68; Conservative 24; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                   T.W.; Seo, H.S.; Choi, Y.D.
MBL Data Library, July 1994
leotide sequence of phytochrome
                                                                                                                                                                                                                                                                                                                                                                    Z16118
                75.4%;
72.6%;
Score 772; DB
Pred. No. 1.3e
20; Mismatches
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                   DB 2;
.3e-67;
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                                                                                                                                                                                                                                                                 PID:g516103
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A;Description: The moss Ceratodon purpureus contains and A;Reference number: $58129
A;Reference number: $58120
A;Reference number: $58130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-577 <HUGo
A;Cross-references: EMBL:X89725
C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; phytochromobilin
F;63-574/Domain: phytochrome homology <PHYT>
F;319/Binding site: phytochromobilin (Cys) (covalent) #s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phytochrome No
C;Species: Pices
C;Date: 20-Sep-C;Accession: T14
R;Clapham, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, June 1996
A; Description: Phytochrome from Picea abies, cDNA complete. A; Reference number: Z18234
A; Accession: T14842
A; Accession: T14842
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1136 <CLA>
A; Residues: 1-1136 <CLA>
A; Rosidues: 1-1136 <CLA>
A; Rosidues: 1-1136 <CLA>
CLA>
CLA>
C; Superfamily: phytochrome; phytochrome homology
C; Keywords: chromoprotein; photoreceptor; phytochromobilin
F: 69-595/Domain: phytochrome homology <CHY>
F: 69-595/Domain: phytochrome homology 
                                                                                                                                                                                                                                                                                                                     phytochrome - moss (Ceratodon purpureus) (fragment) C;Species: Ceratodon purpureus C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 C;Accession: SSB130 R;Hughes, J.; Mittmann, F. submitted to the EMBL Data Library, July 1995 submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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;Species: Picea ables (Norway spruce)
;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
;Accession: T14842
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Best Local :
Query Match
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68.9%;
74.68;
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Pred. No. 5.5e-67;
Score 763.5;
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Best Local
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phytochrome - Martens's spike moss (Species: Selaginella martensii (Martens's spike moss) (Species: Selaginella martensii (Martens's spike moss) (C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_chac;Accession: S31280; S25401 R;Hanelt: S.; Braun, B.; Marx, S.; Schneider-Poetsch, H.A.W. Photochem. Photobol. 56, 751-758, 1992 Photochem. Photochrome evolution: a phylogenetic tree with the A;Title: Phytochrome evolution: a phylogenetic tree with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin;
E;76-588/Domain: phytochrome homology <PHYT>
F;333/Binding site: phytochromobilin (Cys) (covalent) #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-1129 <HEY>
A;Cross-references: GB:S51538; NID:g261208; PIDN:AAB24397.1; PID:g261209
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Heyer, A.; Gatz, C.
Plant Mol. Biol. 20, 589-600, 1992
Plant Mol. Biol. 20, 589-600, 1992
A;Title: Isolation and characterization of a cDNA-clone
A;Reference number: S28431; MUID:93081720
A;Accession: S28431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phytochrome B - potato
C;Species: Solanum tuberosum (potato)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 11-Jun-1999
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Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPHGCHAQYMANMGSIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                      416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 763.5; E
Pred. No. 8.6e-
18; Mismatches
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-368 <MARN
A;Residues: 1-368 <MARN
A;Cross-references: EMBL:U22458; NID:g726314; PID:g726315
C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; photorceeptor; phytochromobilin
E;244/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Reference number: S31280; MUID:93117303
A;Accession: S31280
A;Accession: S31280
A;Molecule type: DNA
A;Residues: 1-1134 <HAN>
A;Residues: 1-1134 <HAN>
A;Cross references: EMBL:X61458; NID:922602; PIDN:CAA43698.1; PID:922603
A;Cross references: EMBL:X61458; NID:922602; PIDN:CAA43698.1; PID:922603
A;Note: the authors translated the codon CTG for residue 239 as Arg, CAC
R;Schneider-Poetsch, H.A.W.; Braun, B.
Plant Physiol. 137, 576-580, 1991
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A; Accession: T09496
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R;Marshall, K.A.; Neale, D.B.
submitted to the EMBL Data Library, March 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phytochrome - Douglas fir (fragment)
C;Species: Pseudotsuga menziesii (Douglas fir)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
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C;Superfamily: phytochrome, phytochrome homology
C;Keywords: chromoprotein; photoreceptor; phytochromobilin; transcription
F;66-582/Domain: phytochrome homology <PHYT>
F;324/Binding site: phytochromobilin (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Proposal on the nature of phytochrome action based on the C-terminal sequences A;Reference number: S25401
A;Recession: S25401
A;Molecule type: mRNA
A;Residues: 'L',730-899,'GLHPP',905-936,'T',938-1134 <SCH>
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C; Genetics:
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Matches 139
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Best Local Similarity
Matches 142; Conserv
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                                                                                                                                                                                                              Local Similarity
les 139; Conserv
                                                                                                                1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60
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                                                                                                                                                                                                            72.9%; Score 746; DB 2; 166.8%; Pred. No. 1.2e-65; tive 22; Mismatches 35;
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Pred. No. 3.6e-65;
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GCHTQYMANMGSVASLALAIVVKGKDSS--------KLWGLVVGHHCSPRYVPFPL 168
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Search completed: June Job time: 208 sec 7, 2002, 18:56:34

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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 KLAVRAISRLQSL
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen
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                                                                                                                                                                                                                                                                   sp_unclassified:*
sp_rvirus:*
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sp_archeap:*
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sp_virus:*
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09m6p6 lycopersico
024380 solanum tub
09zs62 lycopersico
024117 nicotiana p
09sws6 lycopersico
09fpq3 populus tri
09fqw4 averrhoa ca
09fqw4 averrhoa ca
09fqw6 averrhoa ca
09xh84 sporobolus
09fqr5 mortonia gr
09fqr5 mortonia gr
09fqr9 perrottetia
09fqp1 salaciopsis
09xh94 pariana rad
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78.3	78.3	78.3	78.3	78.3	8.4	78.4	78.4	78.4	78.5	78.5	78.5	78.5	78.5	78.5	78.6	78.6	78.6	78.7 1	78.7	78.7	79.0	79.0	79.1	79.1	79.2	79.2	811 79.2 245	79.3	
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Q9fqp7 rei					. Q9fqq1 psa						Q9fqr1 pax							Q9fpq2 pop									Q9fqp5 sal		
reissantia		wimmeria ac	afrostyrax	putterlicki	psammomoya	loeseneriel	cuervea kap	pori	olyra latif	anomochloa		paxistima c	paxistima c	gymnosporia	panicum cap	danthoniops	es	populus tri	D)	eucryphia b	hakonechloa	ripterygi	lithachne p	mortonia gr	ct	salacia imp	salacia imp	ıpia glab	

ALIGNMENTS

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RESULT
Q9M6P6
      Pfam; PF01590; GAF; 1.
Pfam; PF002518; HATPase_C; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; HiskA; 1.
SMART; SM00091; PAS; 2.
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Q9M6P6;
Q1-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                             Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., Pratt L.H.;
"The phytochrome gene family in tomato and the rapid differential evolution of this family in angiosperms.";
Mol. Biol. Evol. 17:362-373(2000).
EMBL, Ref18871; AAF25812.1; -.
EMBL; AF178871; AAF25812.1; -.
InterPro; IPR003018; GAF.
InterPro; IPR003594; HATPase_C.
InterPro; IPR003561; His_kinA.
InterPro; IPR004359; HATS_KIN_sig.
InterPro; IPR004359; HAS_KIN_Sig.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20188796; PubMed=10723737;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Lycopersicon esculentum (Tomato).
Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel.) (TrEMBLrel.
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19,
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Last annotation update)
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Best Local Sin
Matches 165;
                   Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASe_C; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                  InterPro; IPR000977; DNA_ligase.
InterPro; IPR003018; GAF
InterPro; IPR003594; HATPase_c.
InterPro; IPR003561; His_kinA.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR004014; PAS.
InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            024380;
024380;
01-JAN-1998
01-JAN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
SEQUENCE
                                                                                                   Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                            STRAIN-CV. DESIREE; TISSUE-LEAF; MEDLINE-93081720; PubMed-1450376;
                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. DESIREE;
Gatz C.;
                                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum (Potato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                               Plant
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                        PHYB.
                                                                                                                                                                                                                                                                 Heyer A., Gatz
                                                                                                                                                                                                                                                                                                                        Submitted (AUG-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHYTOCHROME
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-4113;
                                                                                                                                                                                                                                                       'Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
                                                                                                                                                                                                                                         phytochrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQLNMELQLASQLAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLAVRSISRLQSLPGGDIGVLCDTAVEDVQKLTGYDRVMVYKFHDDNHGEIVSEIRRSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQLQMELQLASQLAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNAQPVKVVQSEELKQPICLVNSTLRSPH
                                                                                                                                                                                                                     Mol. Biol. 20:589-600(1992). Y14572; CAA74908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
PS00697;
PS00245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00245; PHYTOCHROME_1; 1. PS50046; PHYTOCHROME_2; 1. 1137 AA; 126259 MW; DF
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3 (TrEMBLrel.
1 (TrEMBLrel.
E B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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DNA_LIGASE_A1;
PHYTOCHROME_1;
                                                                                                                                                                                                                                                                                                                                                TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            05,
05,
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Last sequence update)
Last annotation update)
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Pred. No. 1e-8
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
 UNKNOWN_1.
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No. 1e-83;
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                                                                                                                                                                                                                                                                                                                         databases
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                                                                                                                                                                                                                                                     potato
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RESULT
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SQ
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Best Local Similarity 77...
Matches 158; Conservative
       Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM000387; HATPasse_C; 1.
SMART; SM00380; HiSRA; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS000697; DNA_LIGASE_A
PROSITE; PS000697; DNA_LIGASE_A
                                                                                                                                                                                                                                                                                                                                                                                                  Q9ZS62;
Q9ZS62;
Q1-MAY-1999
01-MAY-1999
01-DEC-2001
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VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                 four mutant alleles.";
Plant Mol. Biol. 38:1137-11.
EMBL; AJ002281; CAA05293.1;
                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
PHYTOCHROME B1.
                                                                                                        Pfam; PF02518; HATPase_c;
                                                                                                                  Pfam; PF01590; GAF;
                                                                                                                               InterPro;
                                                                                                                                                                                                                                                 Lazarova G.I., Kubota T., Frances S., Peter Brandstaedter J., Szell M., Matsui M., Ken Cordonnier-Pratt M.M., Pratt L.H.; "Tomato PHYB1: Sequence and identification
                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                PHYB1
                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99084764; PubMed=9869419;
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4081;
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                                                                                                                                                                                   InterPro;
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                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CEFLMQAFGLQLNMELQLASQLSEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPH
                                                                                                                                                 PS50046;
687
695
794
839
 PS00245;
                                                                                                                              IPR001294; Phytochrome IPR002114; PTS_HPr_ser.
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687 N -> T.
695 K -> N.
794 R -> K.
839 P -> T.
                                                                                                                                                                                                                             38:1137-1146(1998).
DNA_LIGASE_A1;
PHYTOCHROME_1;
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77.18;
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                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence up
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Pred. No. 9.2e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
          UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09D1B8375B609584 CRC64;
                                                                                                                                                                                                                                                                       Peters J.L.,
Kendrick R.
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on update)
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Best Local
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Pfam; PF02518; HATPASE_C; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00989; PAS; 2.
Pfam; PF00980; phytochrome; 1.
Pfam; PF00512; Signal; 1.
Prints; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00388; HisKA; 1.
SMART; SM00386; PAC; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
SMART; SM00091; PAS; 2.
PROSITE; PS00097; DNA_LIGASE_A1; PROSITE; PS00097; DNA_LIGASE_A1; PROSITE; PS00045; PHYTOCHROME_L; PROSITE; PS00046; PHYTOCHROME_L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. PBHID; TISSUE=LEAR; STRAIN=CV. PBHID; TISSUE=LEAR; STRAIN=CV. PBHID; TISSUE=LEAR; MEDLINE=98079245; PubMed=9418050; Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson M.E., Robson P.R.H., Kraepiel Y., Caboche M., Smith Hudson M.E., Robson M.E., 
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01-JAN-1998
01-DEC-2001
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024117;
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana plumbaginifolia (Leadwort-leaved tobacco). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Esperantophyta; Asgonliophyta; Streptophyta; Pagnoliophyta; Magnoliophyta; Magno
                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001680;
Pfam; PF01590; GAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phytochrome gene: they have elongated elongated as adult plants."; plant J. 12:1091-2101(1997).
EMBL; Y14676; CAA74992.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; IPR003594; HATPASE_C.
; IPR003661; His_kinA.
; IPR004359; HIS_KIN_sig.
; IPR001610; PAC.
; IPR001014; PAS.
; IPR001294; Phytochrome.
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PS00589;
1131 AA
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B (TrEMBLrel. 05, 1
1 (TrEMBLrel. 19, I
E B.
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      ; DNA_LIGASE_A1;
; PHYTOCHROME_1;
; PHYTOCHROME_2;
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PTS_HPR_SER; UNKNOWN_1
A; 125580 MW; F457278
                                                                                                                                                                                                                                                                                                                                                                                                                    Phytochrome.
WD40.
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                                                                   UNKNOWN_1.
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No. 9.
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Best Loc
Matches
Interpro; IPRO02198; ADH_Short.
Interpro; IPRO03018; GAF:
Interpro; IPRO03594; HATPase_c.
Interpro; IPRO03661; His_kinA.
Interpro; IPRO03661; His_kinA.
Interpro; IPRO03661; His_kinA.
Interpro; IPRO04359; HIS_KIN_sig.
Interpro; IPRO01610; PAS.
Interpro; IPRO01294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_C; 1.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00360; Phytochrome.
SMART; SM000865; GAF; 1.
SMART; SM000865; GAF; 1.
SMART; SM000386; HATPase_C; 1.
SMART; SM000386; HATPase_C; 1.
SMART; SM000386; PAC; 1.
SMART; SM00041; PAS; 2.
PROSITE; PS00046; PHYTOCHROME_1; 1.
PROSITE; PS00046; PHYTOCHROME_1; 1.
SEQUENCE 1121 AA; 125308 MW; ED
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01-MAY-2000
01-MAY-2000
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Control of the gene encoding the apoprotein "Characterization of the gene encoding the apoprotein are the second second
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; euasterids I; Solanales; Solanaceae; Solar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Gen. Genet. 261:901-907(1999)
EMBL; AF122901; AAD50631.1; -.
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Kendrick R.E., Ha
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157; Conser
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1135 AA; 125810 MW; D28846F738C7A2D0
              PS00261; ADH_SHORT; UNKNOWN_1.
PS00245; PHYTOCHROME_1; 1.
PS50046; PHYTOCHROME_2; 1.
1121 AA; 125308 MW; ED9EDA
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., Kelmenson P.M., Schreuder
Hanhart C.J., Koornneef M.,
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Pred. No. 1e-7
18; Mismatches
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Best Local S
Matches 156
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InterPro; IPRO03594; HATPASE_C.
InterPro; IPRO04359; HIS_KIN_S19;
InterPro; IPRO01610; PAC.
InterPro; IPRO01610; PAC.
InterPro; IPRO01294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPASE_C; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00312; signal; 1.
PRINTS; PR00133; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00388; HiskA; 1.
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Q9FPQ3;
Q1-MAR-2001
Q1-MAR-2001
Q1-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Populus trichocarpa (Western balsam poplar).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Salicaceae; Populus.
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Pred. No. 2.4e-76;
6; Mismatches 17;
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Submitted (DEC-1999) to the EMBL/G-
EMBL; AF216091; AAG49048.1; -.
InterPro; IPR003018; GAF.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF00360; Phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SWART; SM00065; GAF; 1.
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Q1-MAR-2001 (TrEMBLrel. 16,
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Q1-DEC-2001 (TrEMBLrel. 19,
PHYTOCHROME B (FRAGMENT).
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                                                                                              Simmons M.P., Doyle J.J.;
                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eleurosids I; Oxalidales; Oxalidaceae; Averrhoa.
                              "Phylogeny of the Celastraceae morphology.";
                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                          NCBI_TaxID=28974;
                                                                                                                                                                                                                                                                                                                                                   Averrhoa carambola (Star fruit).
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InterPro; IPR001294; Phytochrome
Pfam; PF01590; GAF; 1.
Pfam; PF00360; Phytochrome; 1.
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Simmons M.P., Clevinger C.C.,
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PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
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Clevinger
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the EMBL/GenBank/DDBJ
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21; Mismatches 21;
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RESULT
Q9XH84
ID XH84
O9XH87
DT 007
DT 007
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OCC
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                                                                                                                                                                                                       "Phylogenetic structure in the grass family (Poaceae): evi
the nuclear gene phytochrome B.";
L Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF137327; AAD41315.1; -
InterPro; IPR000977; DNA_1igase.
R InterPro; IPR003018; GAF.
R InterPro; IPR003018; GAF.
R InterPro; IPR001294; Phytochrome.
R Pfam; PF01590; GAF; 1.
R Pfam; PF00360; phytochrome; 1.
R PRINTS; PR01033; PHYTOCHROME.
R SMART; SN00065; GAF; 1.
  Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01590; GAF; 1.
Pfam; PF00360; phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SW00065; GAF; 1.
PROSITE; PS00697; DNA_LIGASE_A1; UPROSITE; PS0066; PHYTOCHROME_2; 1
NON_TER 1
NON_TER 365
SEQUENCE 365 AA; 40359 MW; B46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9XH84;
Q9XH84;
01-NOV-1999
01-NOV-1999
01-DEC-2001
                                                                   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sporobolus giganteus.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl. Chloridoideae; Eragrostideae; Sporobolus.
                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Mathews S.Y., Tsai R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF216092; AAG49049.1; -.
InterPro; IPR000977; DAM_IIgase.
InterPro; IPR003018; GAF_
InterPro; IPR001294; Phytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=96053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KLAVRAISQLQLLPGGDIKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRPDL
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                                                                                                                                       PS00697; DNA_LIGASE_A1;
PS00245; PHYTOCHROME_1;
PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 12) (TrEMBLrel. 12) (TrEMBLrel. 12) (TrEMBLrel. 15) B (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                      ΑA;
                                                                      43566 MW;
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    79.68;
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Pred. No. 2.3e
L9; Mismatches
    Score
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                                                                      119CABF4CFDD4B13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            grass family (Poaceae): evidence
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                                                                                                                                                                                      UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E.A.;
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No. 2.
    815;
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2.3e-76;
es 23;
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    10;
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Length 393
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Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1999) to the EMBL/Ge EMBL; AF216087; AAG49044.1; -. InterPro; IPR003018; GAF: InterPro; IPR001294; Phytochrome. Pfam; PF01590; GAF; 1. Pfam; PF01590; GAF; 1. Pfam; PF00360; phytochrome; 1. PRNTS; PR01033; PHYTOCHROME. SMART; SM00065; GAF; 1. PROSITE; PS00245; PHYTOCHROME_1; 1. PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9FQW3;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afrostyrax sp. 'Cheek 5007 K'.
Eukaryota; Viridiplantae; Etteptophyta; Embryo
Spermatophyta; Magnollophyta; eudicotyledons;
eurosids I; Huaceae; Afrostyrax.
NCBI_TaxID-85715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TremBLrel. 16, 01-MAR-2001 (TremBLrel. 16, 01-JUN-2001 (TremBLrel. 17, PHYTOCHROME B (FRAGMENT)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             morphology.
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                                                                          132
                              173
                                                                                                                     121
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KLAVRAISQLRSLPGGDIKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRSDL
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                                                                      GCHTQYMANMGSVASLALAIVVKGKD-----SSKLWGLVVGHHCSPRYVPFPLRYAC 172
                                                                                                                                                                                  EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCHTQYMANMGSVASLALA----IVVKGKDSS------KLWGLVVGHHCSPRYVPFPL
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                                                                                                                                                                                                                                                                                                                                                   156;
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245 AA;
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27112 MW;
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76.58;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                      Score 813; DB 10;
Pred. No. 3.7e-76;
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9; Mismatches 21;
                              196
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edons; core e
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eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                             245;
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Matches 152
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Q9FQR5;
01-MAR-2001
01-MAR-2001
01-JUN-2001
Perrottetia ovata.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Celastraceae; Perrottetia.

NCBI_TaxID=123447;
                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, PHYTOCHROME B (FRAGMENT).
                                                                                                                                                                                                                                Q9FQQ9;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids I; Celastraceae; Mortonia.
NCBI_TaxID=123436;
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PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1
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Doyle J.J.;
                                                                                                                       PHYB.
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Pfam; PF00360; phytoc
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InterPro; IPR001294; Phytochrome.
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245 AA;
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Clevinger
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b; Pred. No. 3.7e
23; Mismatches
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Last sequence
Last annotation
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.7e-76;
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EMBL; AF216143; AAG49100.1; -
InterPro; IPR003018; GAF.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF00360; phytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SN00065; GAF; 1.
                                                              Submitted (DEC-1999) to the EMBL/GIEMBL; AF216165; AAG49122.1; -.
InterPro; IPR003018; GAF.
InterPro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF00360; Phytochrome; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salaciopsis glomerata.
Eukaryota; Viridiplantae;
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Doyle J.J.;
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Doyle J.J.;
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                       PS00245; PHYTOCHROME_1; PS50046; PHYTOCHROME_2;
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InterPro; IPR003018; GAR:
InterPro; IPR003018; GAR:
InterPro; IPR001294; Phytochrome.
Pfam; PF001509; GAR: 1.
Pfam; PF00360; Dhytochrome; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
PROSCETTER: DE001607: DNA ITGREE AL: INKNOWN 1
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Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Arundinoideae; Arundineae; Molinia.
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            EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCIVNSTLRAPH 120
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                                                 KLAVRAISRLQALPGGDVKLLCDTVVENVRELTGYDRVMVYRFHEDEHGEVVAESRRADL
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                                                                                               Similarity 74.(
54; Conservative
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Pfam; PF00989; PAS; 2.
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SMART; SM00065; GAF; 1.
SMART; SM00087; HATPBASE_C; 1.
SMART; SM00388; HISKA; 1.
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PROSITE; PS50109; HIS_KIN; 1.
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ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOFENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES, PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN.

BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN.

PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
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InterPro; IPR003594; HATPase_C.
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PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROL

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMER

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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PF02518; HATPase_c; 1.
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PS00245;
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PHYTOCHROME_1;
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PAS 2.

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CHROMOPHORE (BY SIMILARITY).

CHROMOPHORE (BY SIMILARITY).
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RA Zheng C.C., O'Neill S.D.;

RA Zheng C.C., O'Neill S.D.;

RL Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

RL Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.

CC -1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABSORBS

CC ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PER FORM THAT ABSORBS

CC MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN CC ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN CC PRINCESS AN ARRAY OF MORPHGENIC RESPONSES, WHEREAS

CC RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-CC BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN.

CC PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS

THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
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PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                    European Bioinformatics Institute.
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IPR003661; His_kinA.

IPR003018; GAF

InterPro;

InterPro; IPR000014; PAS. InterPro; IPR001294; Phytochrome.

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Wiegmann Eirund C.M., Kolukisaoglu H.U.;
Wiegmann Eirund C.M., Kolukisaoglu H.U.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.

1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABSORBS ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE FED REGION. PHOTOCONVERSION OF PR IN ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCTION OF THOSE RECONVERSION OF PR OF CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHY_PINSY Q41046;
                                                                                                                                                                                                                                                                                                                              Pinus sylvestris (Scots pine)
Eukaryota; Viridiplantae; Str
Spermatophyta; Coniferopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
01-MAR-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
SEQUENCE
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DOMAIN
                                                                                                                                                                                                                                           STRAIN-PSA 5.1;
                                                                                                                                                                                                                                                                  SEQUENCE FROM
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SM00387; HATPase_c; 1.

SM00388; Hiska; 1.

SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCHTKYMANMGSIASLVMAVVINSSESMKLWGLVVCHHTSPRYVPFPLRYACEFLMQAFS
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672
732
880
318
1115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AΑ;
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; PAC; 1.
; PAS; 2.
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41,
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728
803
1100
318
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PHYTOCHROME_2;
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87.2%;
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PAG 2.
PAS 2.
HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY).
MW; 081A4154EE147800 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        pine).
                                                                                                                                                                                                                                                                                                                              Streptophyta; Embryophyta; Tracheophyta; ida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence up
annotation
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.7e-85;
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Best Local Sin
Matches 160;
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InterPro; IPRO01294; Phytochrom
Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00519; PAS; 2.
Pfam; PF00519; PAS; 2.
Pfam; PF00512; Signal; 1.
Pfam; PF00512; Signal; 1.
Pfam; PF00512; Signal; 1.
PATANTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
DECOITE SECTION OF TAXES.
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DOMAIN
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                              Repeat.
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InterPro;
InterPro;
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InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                        Transcription
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391
                       172
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                                                                                                                                                                 1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
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PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN

SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FI
            CEFLMQAFGLQLQMELQLASQLAEK
                                                                                                             EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
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 CEFLMQALGLQLNMELQLAAQLTEK
                                                GCHAQYMANMGSIRSLLMAVIINGNDDEGGGSGRNSMKLWGLVVCHHTSPRAVPFPLRYA
                                                             GCHTQYMANMGSVASLALAIVVKGKD------
                                                                                                 EPYLGLHYPATDIPQASRFLFMQNRVRMICDCMATPVKVIQSEELMQPLCLVGSTPSAPH
                                                                                                                                                 KLAVRAISRLQSLPCGDVGLLCDTVVENVRELTGYDRVMVYKFHEDEHGEVVAEIRRSDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X96738; CAA65510.1; -.
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                 PS50109; HIS_KIN; 1.
PS50112; PAS; 2.
PS00245; PHYTOCHROME_1;
PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig.
IPR003661; His_kinA.
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                                                                                                                                                                                                                                                              621
755
903
332
1131
                                                                                                                                                                                                 Conservative
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332
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78.0%;
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                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                    PAS 1.
PAS 2.
HISTIDINE
                                                                                                                                                                                                                                                           HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY).
MW; D63A2008FA9862FB CRC64;
                        196
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                             840.5;
No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                         ; DB 1,
2.9e-77;
21;
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                                                                       SSKLWGLVVGHHCSPRYVPFPLRYA
                                                                                                                                                                                                                                                                                                                                      Phytochrome;
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SO CONTROLS
FEEDBACK FA
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                                                                                                                                                                                                                                                                                                                                        Chromophore;
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RESULT 4
PHYB_TOBAC

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PHYB_TOBAC
P29130;
01-DEC-1992
01-FEB-1994
01-MAR-2002
PRINTS;
SMART; S
SMART; S
SMART; S
SMART; S
SMART; S
                                                                                                                                                                                                                                                         EMBL; L10114;
EMBL; M65023;
Mendel; 1321;
                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                 This
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PIANT CALL 4:241-251(1992).

ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORB MAXIMALLY IN THE REGION OF THE SPECTRUM AND THE PFR FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHICAROPHYLL A/B BINDIAM PROTECHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                           InterPro;
                                                                                                                                                                     InterPro; IPR003018; GAF.
InterPro; IPR003594; HATPase_c.
InterPro; IPR004359; HIS_KIN_sig.
InterPro; IPR003661; His_kinA.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
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Kendrick R.E., Furu
"The cucumber long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92361250; PubMed=1498594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-94105358; PubMed-8278560;
Kern R., Gasch A., Deak M., Kay S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "рһув
                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER.

PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN

SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                               n; PF01590; GAF; 1.
n; PF02518; HATPASe_c; 1.
n; PF00380; PAS; 2.
n; PF00380; phytochrome; 1.
n; PF00512; signal; 1.
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of tobacco, a new
  SM00065; G
SM00065; G
SM00387; H
SM00388; H
SM00086; P
SM00091; P
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                                                                                                                                                                                                                                                                                                             the Swiss Institute or pean Bloinformatics Institute. The pean Bloinformatics Institutions as long and this statement is not removed. In requires a license agreement (See
                                                                                                                                                           IPR001294;
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(Rel.
(Rel.
B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457-1132 FROM N.A
                                                                                                                                                                                                                                                         NICta; PhyB; 1.
                                                                                                                                                                                                                                                                    AAA34092.1; -.
AAA34093.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Furuya M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagatani A., Tomizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                           HATPase_c;
                                                        GAF; 1.
                              HisKA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Common tobacco)
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                                                                                                                                                         Phytochrome.
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member of
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                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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Best Local
"The SOLYAUM."---
phytochrome B.";
Plant Physiol. 113:611-619(1997).

Plant Physiol. 113:611-619(1997).

Plant Physiol. 113:611-619(1997).

Plant Physiol. 113:611-619(1997).

PUNCTION: REGULAMORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT AB MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF THOSE PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
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BINDING
CONFLICT
CONFLICT
SEQUENCE
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16-OCT-2001
16-OCT-2001
01-MAR-2002
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DOMAIN
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PROSITE;
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MEDLINE=97198556; PubMed=9
Childs K.L., Miller F.R.,
Morgan P.W., Mullet J.E.;
                                                                                                                                                                                                                                                                                                                                                           Alba R., Kelmenson P.M., Cordonnier-Pratt M.-M., "The phytochrome gene family in tomato and the ratevolution of this family in anglosperms."; Mol. Biol. Evol. 17:362-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. 58M; MEDLINE=20188796; PubMed=10723737;
                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sorghum bicolor (Sorghum) (Sorghum v
Eukaryota; Viridiplanthee; Streptophy
Spermatophyta; Magnoliophyta; Liliop
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00245; PHYTOCHROME_1; PROSITE; PS50046; PHYTOCHROME_2; Transcription regulation; Photor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHYB OR MA3.
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PS50112;
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PAS; 2.
                                                                                                                                                                                                                                                                        PubMed=9046599;
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41,
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Last
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                                                                                                                                                                                                                                               Cordonnier-Pratt M.-M., Pratt L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Sorghum vulgare).
Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; PACC clade;
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PAS 2.
PAS 2.
HISTIDINE KINASE.
HISTIDINE (BY SIMILA
L-> S (IN REF. 2).
L-> LO (IN REF. 2).
MW: 457F09C024C0F608 C
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Pred.
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No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1178
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.4e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                      f.-M., Pratt L.H.;
the rapid differential
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Matches
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Best Local
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Interpro; IPR003661; HiS_KINA.
Interpro; IPR00314; PAS.
Interpro; IPR001294; Phytochrome.
Pfam; PF01590; GAF; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; Phytochrome; 1.
Pfam; PF00360; Phytochrome; 1.
Pfam; PF00371; Signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; HISKA; 1.
SMART; SM00388; HISKA; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50146; PHYTOCHROME_1; 1.
PROSITE; PS50146; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).

-! SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

-!- SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

-!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; Photoreceptor; Phytochrome; Chromophore; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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431
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                                      169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR. GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
                                                                                                                                                                                                                                                                                   KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60
                                                                                                          GCHTQYMANMGSVASLALAIVVK--GKD----
                  RYACEFLMQAFGLQLQMELQLASQLAEK
                                                                                                                                                                                            EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATFVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                          KLAVRAISRLQALPGGDIKLLCDTVVEHVRELTGYDRVMVYRFHEDEHGEVVAESRRDNL 310
                                                                                 GCHAQYMANMGSIASLVMAVIISSGGDDEQTGRGGISSAMKLWGLVVCHHTSPRCIPFPL
                                                                                                                                                                   EPYLGLHYPATDIPQASRFLFRQNRVRMIADCHATPVRVIQDPGMSQPLCLVGSTLRAPH
                                                                                                                                                                                                                                                                                                                                                     153;
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
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23
43
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1170
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73.6%;
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Pred. No. 9.6e
21; Mismatches
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POLY-HIS.
POLY-GLY.
CHROMOPHORE (BY SIMILARITY).
CHROMOPHORE (BY SIMILARITY).
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PAS
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.6e-74;
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RESULT 6
PHYB_ARATH
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P14713;
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Moffat K.S., Cronin L.A., Shen M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                              NATURE 402:761-768(1999).

NATURE 402:761-768(1999).

PUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABSORBS ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBURIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed J.W., Nagpal P., Poole D.S., Furuya M., Chory J.;
"Mutations in the gene for the red/far-red light receptor phytochrome
B alter cell elongation and physiological responses throughout
Arabidopsis development.";
                                                                                                                 the
                                                                                                                                                                         This
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phytochrome B. Phytochrome B. Phyto OR HY3 OR AT2G18790 OR MSF3.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1990
01-MAR-2002
entities requires a license agreement (Some send an email to license@isb-sib.ch).
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STRAIN=CV. LANDSBERG ERECTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Novel phytochrome sequences in Arabidopsis thaliana: structure, evolution, and differential expression of a plant regulatory photoreceptor family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90108670; PubMed=2606345; Sharrock R.A., Quail P.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV.
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                                                                                                                                                                                                                                                                                                                                             <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Sequence and analysis of chromosome 2 of the
                                                 ween the Swiss Institute of Bioinformatic
European Bioinformatics Institute. Then
by non-profit institutions as long
ified and this statement is not removed.
                                                                                                                                                                                                                              PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE. SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY. SIMILARITY: CONTAINS 2 PAS (PER-ARMY-SIM) DIMERIZATION DOMAINS. SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER.
                                                                                                                                         SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell 5:147-157(1993).
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V. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 14,
(Rel. 14,
(Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3:1745-1757(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8453299;
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                       http://www.isb-sib.ch/announce/
                                                       Usage
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RESULT
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SMART; SM00387; HAFPEASE_C; 1.
SMART; SM00388; HiskA; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50046; PHYTOCHROME_1; 1
PROSITE; PS50046; PHYTOCHROME_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; Phytochrome; 1.
Pfam; PF00512; signal; 1.
PRINTS; PR01033; PHTTOCHROME.
                                                                                                                                                                                      PHYB_ORYSA STANDARD
P25764;
01-MAY-1992 (Rel. 22, C
01-MAY-1992 (Rel. 22, I
01-MAR-2002 (Rel. 41, I
Phytochrome B.
                                                           Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                        ORYSA
  STRAIN-CV.
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BINDING
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                      SEQUENCE FROM N.A.
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InterPro; IPR003594; HAMPBASe_C.
InterPro; IPR004359; HIS_KIN_Sig.
InterPro; IPR003661; His_KinA.
InterPro; IPR000014; PAS.
InterPro; IPR001294; Phytochrome.
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; AC005724; AAD08948.1; -.
507718; FKMUB.
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el; 1310; ARAth;
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652 723
786 857
934 1153
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  INDICA-IR36;
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1172
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72.98;
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TISSUE-Seedling
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Pred. No. 2.2e
23; Mismatches
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PAS 2.
HISTIDINE KINA
GLY/SER-RICH.
CHROMOPHORE.
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  shoot
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ies 22;
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243 61

EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH

120 302 60 Query Match Best Local S Matches 150

Similarity

Conservative

23;

Indels

13;

Gaps

2

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Dehesh K., Tepperman J., Christensen A.H., Quail P.H.;

"phyB is evolutionarily conserved and constitutively expressed in

"rice seedling shoots.",

"Mol. Gen. Genet. 225:305-313(1991).

"L. Mol. Gen. Genet. 225:305-313(1991).

"C. -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT

ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS.

"C. MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT

ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN

"C. PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS."

RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE

RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR

GENES INCLUDING THOSE ENCODING THE SMALL SUBJUNIT OF RIBULOSE-

"BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,"

PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS

THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                       Pfam; PF01590; GAF; 1.

Pfam; PF02518; HATPase_C; 1.

Pfam; PF00989; PAS; 2.

Pfam; PF00360; phytochrome; 1.

Pfam; PF00512; signal; 1.

PFINTS; PR01033; PHYTOCHROME.

SMART; SM00065; GAF; 1.

SMART; SM00087; HATPase_C; 1.

SMART; SM00091; PAS; 2.

SMART; SM00091; PAS; 2.
                                                                                         BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                                                            Transcription regulation; Photoreceptor; Repeat; Multigene family.

DOMAIN 661 732 PAS 1.

DOMAIN 795 866 PAS 2.

DOMAIN 943 1161 HISTIDINE KI
                                                                                                                                                                                                                                   PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS00245; PHYTOCHROME_1;
PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mendel; 1319; ORYSa;PhyB;1.
InterPro; IPR003018; GAF.
InterPro; IPR003594; HATPase_c.
InterPro; IPR004359; HIS_KIN_Sig.
InterPro; IPR003661; HiS_KinA.
InterPro; IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X57563; CAA40795.2; -. PIR; S14065; S14065.
                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91172131; PubMed=2005872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMODIMER.

SUBUNIT: HOMODIMER.

PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001294; Phytochrome.
                                                                                          AA;
                                                                                                                             866
1161
51
                                                                                         364
.; 128384
                 77.6%;
                                                                                          Μ.,
Score 794.5; DB 1;
Pred. No. 1.4e-72;
3; Mismatches 23;
                                                                                                                                            PAS 1.
PAS 2.
HISTIDINE KINASE.
                                                                                         CHROMOPHORE (BY SIMILARITY)

W; E8292E88B769BF16 CRC64;
                                                                                                                              POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ong as its content is in
                                                                                                                                                                                                                    Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIMERIZATION DOMAINS
                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
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PHYD_ARATH
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                                                                                                                                                                                     RX MEDLINE-98121131; Nebmed-9461215;
RX MEDLINE-98121131; Nebmed-9461215;
RA Beryah M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Beryah M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,
RA Beryah M., Bancroft I., Wan Strevenen M., Strekema W., Drost L.,
RA Glelen J., Villarroel R., Weitzenegger T., Pohl T.M., Terryn N.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Gielen J., Villarroel R., De Clerck R., van Montagu M., Lecharny A.,
RA Gielen J., Rees M., Lao N., Kavanagh T., Hempel S., Kotter P.,
RA Silvey M., James R., Montfort A., Pons A., Pulgdomenech P., Douka A.,
RA Silvey M., James R., Montfort A., Pons A., Pulgdomenech P., Douka A.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
RA Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
Ra Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,
Ra Palme K., Benes V., Rechman S., Ansorge W., Cooke R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P42497; 023472;
01-NOV-1995 (Rel.
16-OCT-2001 (Rel.
01-MAR-2002 (Rel.
Phytochrome D.
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94325466; PubMed=8049367;
Clack T., Mathews S., Sharrock R.A.;
"The phytochrome apoprotein family in Arabidopsis is
genes: the sequences and expression of PHYD and PHYE.
Plant Mol. Biol. 25:413-427(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. COLUMBIA; PumEDLINE=98121113; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV. LANDSBERG MEDLINE=94325466; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                  SUBUNIT: HOMODIMER.

PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRYACEFIMQAFGIQIQMEIQIASQIAEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCHGQYMANMGSIASLVMAVIISSGGDDDHNIARGSIPSAMKLWGLVVCHHTSPRCIPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPYIGLHYPATDIPQASRFLFRQNRVRMIADCHAAPVRVIQDPALTQPLCLVGSTLRSPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERECTA;
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Last annotation update)
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  ne EMBL outstation restrictions on in
                                           a collaboration
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RESULT PHYB_SO

SOYBN

9

PHYB_SOYBN

STANDARD;

PRT;

1156

A

OCCUPTION

PHYB.

Eukaryota; Viridiplantae; Spermatophyta; Magnoliophy Glycine max (Soybean)

Magnoliophyta;

Streptophyta; Embryophyta; rta; eudicotyledons; core e

eudicots;

Tracheophyta;

P42499; 01-NOV-1995 01-NOV-1995 01-MAR-2002

5 (Rel. 32, Created)
5 (Rel. 32, Last sequence of the control of t

sequence update)
annotation update;

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 멍
                                                                                                                                                                                            Matches 148;
                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR003594; HATPase_C.
Interpro; IPR004359; HIS_KIN_sig.
Interpro; IPR004359; HIS_KINA.
Interpro; IPR000361; His_KinA.
Interpro; IPR000014; PAS.
Interpro; IPR001294; Phytochrome.
Pfam; PP01590; GAF; 1.
Pfam; PF002518; HATPase_C; 1.
Pfam; PF00360; Phytochrome; 1.
Pfam; PF00398; PAS; 2.
Pfam; PF00512; Signal; 1.
PRINTS; PR01033; PHYTOCHROME.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; HATPase_C; 1.
SMART; SM00388; HATPase_C; 1.
SMART; SM00388; HATPase_C; 1.
SMART; SM00388; HATPase_C; 1.
                                                                                                                                                                                                                                                              Repeat; Multigene f
DOMAIN 656
DOMAIN 790
DOMAIN 938 1
BINDING 360
CONFLICT 425
                                                                                                                                                                                                                                                      BINDING
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 297340; CAB10404.1;
EMBL; AL161543; CAB78667.1
Mendel; 7189; ARAth; PhyD;1
Mendel; 26747; Arath; PhyD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X76609;
                                                                                                                                                                                                                                                                                                                                        Franscription
                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00245; PHYTOCHROME_1; PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
 419
                       169
                                               359
                                                                    121
                                                                                             299
                                                                                                                                            239
                                                                                                                                                                                                      Local Similarity
                                                                                                                     61
                                                                                                                                                         1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
RYACEFLMQAFGLQLNMELQLALQVSEK
                                                          EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
                       RYACEFLMQAFGLQLQMELQLASQLAEK
                                               GCHAQYMTNMGSIASLAMAVIINGNEEDGNGVNTGGRNSMRLWGLVVCHHTSARCIPFPL
                                                                                             EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCYASPVRVVQDDRLTQFICLVGSTLRAPH
                                                                                                                                            KLAVRAISHLQSLPSGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRNDL
                                                                                                                                                                                                                                                                                                                                                                         PS50109;
PS50112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6747; Arath; PhyD; 26747
IPR003018; GAF.
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                        regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA54072.1; -.
                                                                                                                                                                                                                                                                                                                                                                         ; PAS; 2.
09; HIS_KIN;
12; PAS; 2.
                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAB78667.1; -.
                                                                                                                                                                                                                                                                family. 727
727
861
1157
1425
                                                                                                                                                                                                       76.5%;
71.2%;
                                                                                                                                                                                                                                                         129267
                                                                                                                                                                                                                                                                                                                                        Photoreceptor;
                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                      CHROMOPHORE (BY SIMILARITY).
L -> F (IN REF. 1).
LW; BB7CFE19C50ACBAB CRC64;
                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                        PAS 1.
PAS 2.
HISTIDINE
                                                                                                                                                                                            Mismatches
 446
                       196
                                                                                                                                                                                                       783; DB 1;
No. 2.1e-71;
                                                                                                                                                                                                                                                                                         KINASE
                                                                    -GKDSSKLWGLVVGHHCSPRYVPFPL
                                                                                                                                                                                                                                                                                                                                       Phytochrome; Chromophore;
                                                                                                                                                                                                                 Length 1164;
                                                                                                                                                                                            Indels
                                                                                                                                                                                            12;
                                                                                                                                                                                            Gaps
                                                                     168
                                                                                                                     120
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Best Local S
Matches 146
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InterPro; IPR003594; HATPase_c.
InterPro; IPR003594; HIS_KIN_sig.
InterPro; IPR003661; His_kinA.
InterPro; IPR000014; PAS.
InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. PALLAL; TISSUE-Etiolated leaf;

STRAIN-CV. PALLAL; TISSUE-Etiolated leaf;

Bahn T.R., Woo T.W., Seo H.S., Chol Y.D.;

Submitted (XXX-1994) to the EMBLYGENBAK/DDBJ databases.

1- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS ANALMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCTS AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBUIOSE-
                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASS_C; 1.
SMART; SM00388; Hiska; 1.
SMART; SM00091; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00360; phytochrome; 1. Pfam; PF00512; signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                            Multigene
                                                                                                                                                                                                                                                                       Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBL_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mendel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
 300
                                                           240
                               64
                                                        European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial ittes requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
SIMILARITY: CONTAINS 1 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER.
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
              LGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION
IGLHYPATDIPQASRELFKQNRVRMIVDCHASAVRVVQDEALVQPLCLVGSTLGAPHGCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : L34843;
el; 8366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                        146;
                                                                                                                                   Similarity
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                                                                                                                                                                                       e family.

646

930

358

3156

AA;
                                                                                                                                                                                                                                                                                        PS50046;
                                                                                                                                                                                                                                                                                                      PS00245;
                                                                                                                                                                                                                                                                                                                      PS50112; PAS;
                                                                                                                       Conservative
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                                                                                                                                                                                                                             717
1150
                                                                                                                                                                                                                                                                                        PHYTOCHROME_1;
PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                    HIS_KIN; 1.
                                                                                                                                75.4%;
72.6%;
                                                                                                                                                                                               129085
                                                                                                                                                                                                                                                                       Photoreceptor; Phytochrome; Chromophore;
                                                                                                                       20;
                                                                                                                                                                                                WW;
                                                                                                                     Score 772; DB
Pred. No. 2.7e
20; Mismatches
                                                                                                                                                                                                           PAS.
HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY)
                                                                                                                                                                                                76333AABDC42D297
                                                                                                                                                                                                                                                                                          2 772; DB 1; L
. No. 2.7e-70;
ismatches 27;
                                                                                                                                                 Length 1156,
                                                                                                                                                                                                CRC64;
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RESULT 10

PMY_PICAB

ID PHY_P AC

Q4076

DT 01-NO

DT 01-NO

DT 01-NO

DT 01-NO

DT 01-NO

CC 01-1-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RA CLapham D.H., LAISSON C.T., Qamaruddin M.;

RA SLADMHILLER (JUL-1996) to the EMBL/GenBank/DDBJ databases.

RI SLADMHILLER (JUL-1996) to the EMBL/GenBank/DDBJ databases.

CO -I- FUNCTION: REGULATORY PHOTORECEPIOR WHICH EXISTS IN TWO FORMS THAT CONTROL THAT THE PERFORM THAT ABSORBS THAT CONTROL THE FER FORM THAT ABSORBS ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PER FORM THAT ABSORBS MAXIMALLY IN THE FER FEED REGION. PHOTOCONVERSION OF PR IN COPE AND ARRAY OF MORPHOGENIC RESPONSES, WHEREAS COMES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS THE INDUCTION OF THOSE RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES, PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR COMES THOSE THOSE MALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.

C-I- SUBUNIT: HOMODIMER (BY SIMILARITY).

C-I- SUBUNIT: BELONGS TO THE PHYTOCHROME FRAMILY.

C-I- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS:

C-I- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                         PROSITE;
PROSITE;
PROSITE;
PROSITE;
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Q40762;
01-NOV-1997
                                                                                                                                    SMART; SM00065; GAF; 1.
SMART; SM00387; HATPASe_C; 1.
SMART; SM00388; HiskA; 1.
SMART; SM00091; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                 Pfam; PF00360; phytochrome; 1. pfam; PF00512; signal; 1. PF10133; PHYTOCHROME.
                                                                                                                                                                                                                                                                                                                                     Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Picea abies (Norway spruce) (Picea excelsa).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
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01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3329;
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                                                         PS00245;
                                                                                                                PS50109;
                            PS50046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000014; PAS.
IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003594; HATPase_c.
IPR004359; HIS_KIN_sig.
IPR003661; His_kinA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003018; GAF
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(Rel.
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                                                   ; HIS_KIN; 1.
; PAS; 2.
; PHYTOCHROME_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 35, Created)
. 35, Last sequence. 41, Last annotation.
                         PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
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Photoreceptor; Phytochrome;

Chromophore;

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RESULT
PHY2_CF
ID PF
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                                                                                                                       RT "GERPU; PHY0; 2, a 'normal' phytochrome in Ceratodon.";
RL [II] Plant Gene Register PGR96-067.
CI FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT CONTROL REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT CONTROLLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT COMMANIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN COMPRESSION OF PR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS COMPERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RECONVERSION OF PR IN CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR COMPROSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-COMPONENTATE CARBOXILASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENES) IN A NEGATIVE FEEDBACK FASHION.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBUNIT: BELONGS TO THE PHYTOCHROME FAMILY.
CC -!- SIMILARITY: CONTAINS 2 PAS (PER-ARNY-SIM) DIMERIZATION DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 HASTIDINE KINASE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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Best Local
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01-NOV-1997
01-NOV-1997
01-MAR-2002
Phytochrome
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BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ceratodon purpureus (Moss).
Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Rr~onsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat.
DOMAIN
DOMAIN
         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CERPU
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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762
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1136
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: 126066 h
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41,
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Pred. No. 1.2e
23; Mismatches
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PAS 2.
HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY).
MW; 07A4E01498453E93 CRC64;
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. No. 1.2e-69;
ismatches 29;
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Best Local S
Matches 140
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pfam; pr005918; HATPASE_C; 1.
pfam; pr003819; phytochrome; 1.
pfam; pr00360; phytochrome; 1.
pfam; pr00512; signal; 1.
pranty; pr01033; pHYTOCHROME.
SMART; SM00085; GAF; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00388; PAG; 1.
SMART; SM00386; pAG; 1.
SMART; SM00091; PAS; 2.
DECOTOR: DECOTOR: TYPE: 1.
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InterPro; IPR003594; HATPASE_C.
InterPro; IPR003593; HIS_KIN_Sig.
InterPro; IPR003661; HiS_kinA.
InterPro; IPR001610; PAC.
InterPro; IPR000114; PAS.
InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Multigene family.

DOMAIN 608 679

DOMAIN 742 813

DOMAIN 893 1113

BINDING 319 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
PROSITE;
PROSITE;
         MEDLINE=93081720; PubMed=1450376;
Heyer A., Gatz C.;
"Isolation and characterization o
                                                                          Solanum tuberosum (Potato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Solanales; Solanaceae; Solanum.
                                                                                                                               PHYB
                                                                                                                                                      01-FEB-1994
01-MAR-2002
                                                                                                                                                                             P34094;
01-FEB-1994
                                                                                                                                                                                                                 SOLTU
                                             SEQUENCE FROM
                                                                 Asteridae; euasterids
NCBI_TaxID=4113;
                                                                                                                                            Phytochrome
                                                                                                                                                                                                     PHYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50046; PHYTOCHROME_2;
                                                                                                                                                                                                                                                                                    172
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                                                                                                                                                                                                                                                                        CEFLMQAFGLQLQMELQLASQLAEK 196
                                                                                                                                                                                                                                                                                                                        GCHTQYMANMGSVASLALAIVVKGKDSS------KLWGLVVGHHCSPRYVPFPLRYA 171
                                                                                                                                                                                                                                                                                                                                                                       EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120
                                                                                                                                                                                                                                                                                                                                                                                                                   KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                                                                                                                                                                                                     SOLTU
                                                                                                                                                                                                                                                               CEFLMQVFGMQLNMEVELAAQLREK
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                                                                                                                                                                                                                                                                                                            GCHAQYMGNMGSIASLVMAVIINDNEEDSRGAIQRGRKLWGLVVCHHTSPRTVPFPLRSA
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phytochrome
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PS50112; PAS; 2.
PS00245; PHYTOCHROME_1;
                                                                                                                                                    (Rel.
(Rel.
(Rel.
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28,
41,
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                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 763.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAS 1.
PAS 2.
HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY)
                                                                                                                                                                                                                                                               402
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
            of.
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           ø
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            cDNA-clone
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           coding
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           for potato
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Best Local :
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Mendel; 10718; SOLtu; PhyB;1.

InterPro; IPR003018; GAF.

InterPro; IPR003594; HATPSSe_C.

InterPro; IPR004359; HIS_KIN_sig.

InterPro; IPR0003661; His_KinA.

InterPro; IPR00014; PAS.

InterPro; IPR001294; Phytochrome.
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; signal; 1
Pfam; PF00512; signal; 1
Pfam; PF00512; signal; 1
Pfam; PF00512; signal; 1
PARITS; PR01033; PHTTOCHROME.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; Hiska; 1.
SMART; SM00388; Hiska; 1.
SMART; SM0091; PAS; 2.
PROSITE; PS50102; PAS; 2.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                              BINDING
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 20:589-600(1992).
                              136
                                                              287
                                                                                                                               227
                                                                                                                                                              16
                                                                                              76
                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER.

FIM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: REGULATORY PHÔTOREĆEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN PER INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PER TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR RESPONSES. PER CONTROLS THE EXPRESSION OF A NUMBER OF RIBULOSE-BISPHOSE HACLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                            LALAIVVKGKD-----SKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFGLQLQME
                                                          LTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYACEFLMQAFGLQLNME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S51538; AAB24397.1; -.
                                                                                                                                                                                                                                                                         ; Multigene family.
622 693
755 826
1 903 1122
1 903 333
1 333 333
1 125621
                                                                                                                                                                                                                                                                                                                                                                                            PS50046; PHYTOCHROME_2;
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                           74.68;
                                                                                                                                                                                                                                                                             125621
                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                             WW;
                                                                                                                                                                                            Score 763.5; |
Pred. No. 1.9e
18; Mismatches
                                                                                                                                                                                                                                                                                                                          PAS
                                                                                                                                                                                                                                                                                          HISTIDINE KINASE CHROMOPHORE.
                                                                                                                                                                                                                                                                             60DF5FB964EFC60B CRC64;
                                                                                                                                                                                          1.9e-69;
hes 21;
                                                                                                                                                                                                                          DB 1;
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                                                                                                                                                                                                                          Length 1129;
                                                                                                                                                                                              Indels
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                              186
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RESULT 13
PHY_ADICA
PHY_ADICA
PHY_ADICA
AC P4249
DT 30-MA
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                                                                                                                                 Pfam; PF01590; GAF; 1.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF00989; PAS; 2.
Pfam; PF00360; phytochrome; 1.
Pfam; PF00512; Signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995
30-MAY-2000
01-MAR-2002
                           PRINTS; PRO1033; PHYTOCHROME.
SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase_C; 1.
SMART; SM00388; HiskA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHY_ADICA P42496;
                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB016168; BAA31856.1; -.
InterPro; IPR003018; GAF.
InterPro; IPR003594; HATPASE_C.
InterPro; IPR004359; HIS_KIN_sig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Filicophyta; Filicopsida; Filicales; Adiantaceae; Adiantum.
NCBI_TaxID-13818;
                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHIC SUBUNIT: HOMODIMER.

PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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                                                                                                                                                                                                                                                                                                IPR003661; His_kinA.
IPR001610; PAC.
IPR000014; PAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Hirano Y., Abe H., Tomizawa K.I., Furuya M., Wada M.; ced amino sequence of phytochrome from Adiantum includes motifs present in phytochrome B from seed plants."; Physiol. 34:1329-1334(1993).
                                                                                                                                                                                                                                                                          IPR001294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TO 28; 93-97; 310; 345 AND 1044.
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                                                                                                                                                                                                                                                                       Phytochrome
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MEDLINE=93117103; PubMed=1475321;

RA Hanelt S., Braun B., Marx S., Schneider-Poetsch H.A.W.;

RT "Phytochrome evolution: a phylogenetic tree with the first complete RT sequence of phytochrome from a cryptogamic plant (Selaginella RT martensii spring).";

RI Photochem. Photobiol. 56:751-758(1992).

CC ARR REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS TO THE RED REGION OF THE SPECTRUM AND THE PR FORM THAT ABSORBS TO ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN THE RED REGION. PHOTOCONVERSION OF PR IN THE RED REGION. PHOTOCONVERSION OF PR IN THE RESONNESS. MERCAS RECONVERSION OF PR CONTROLS THE INDUCTION OF THOSE RESONNESS. PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RAM, ETC. IT ALSO CONTROLS THE EXPRESSION OF THS SHALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN.

PROTOCHLOROPHYLLIDE REDUCTASE, RAMA, ETC. IT ALSO CONTROLS THE EXPRESSION OF THE SUBUNIT: HOMODIMER.

-!- SUBUNIT: HOMODIMER.

-!- SUBUNIT: HOMODIMER.

-!- SIMILARITY: BELONGS TO THE PHYTOCHROME FRAMILY.

-!- SIMILARITY: BELONGS TO THE PHYTOCHROME FRAMILY.
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Best Local Similarity
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01-JUL-1993 (Rel.:
01-JUL-1993 (Rel.:
01-MAR-2002 (Rel.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat.
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           Selaginella martensii (Martens's spike moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Lycopodiophyta; Isoetopsida; Selaginellales; Selaginellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM
PROSITE;
PROSITE;
PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                     Selaginella
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Phytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHY1_SELMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEFLMQVFSLQLNMEVGMAAQVREK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139;
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TE; PS50109;

TE; PS50112;

TE; PS00245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00091; PAS; 2.
; PSS0109; HIS KIN; 1.
; PSS0112; PAS; 2.
; PSS0145; PHYTOCHROME_1; 1
; PSS0046; PHYTOCHROME_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1118
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740
887
317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   26,
26,
41,
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Last annotation update)
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PAS 2.
PAS 2.
HAS 2.
HISTIDINE KINASE.
CHROMOPHORE (BY SIMILARITY).
774 MW; 27C218F61F4B9333 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 758.5; DB
No. 6e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
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ΑC

PHY1_PHYPA P36505;

STANDARD

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Best Local S
Matches 142
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InterPro; IPR003661; His_kinA.
InterPro; IPR001610; PAC.
InterPro; IPR000700; PAS-assoc_C
InterPro; IPR000700; PAS-assoc_C
InterPro; IPR0001294; Phytochrome
InterPro; IPR001294; Phytochrome
Pfam; PP01590; GAF; 1.
Pfam; PF01590; GAF; 1.
Pfam; PF003610; Phytochrome; 1.
Pfam; PF00360; Phytochrome; 1.
Pfam; PF00512; signal; 1.
Pfam; PF00512; signal; 1.
Pfam; PF00512; Signal; 1.
SMART; SM00065; GAF; 1.
SMART; SM00086; HAFPase_C; 1.
SMART; SM00388; HAFPase_C; 1.
                                                                                                                                                                                                                                                                                                                      Repeat;
DOMAIN
DOMAIN
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DOMAIN
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PROSITE; PS50113; PAC; 1.
PROSITE; PS50112; PAS; 2.
PROSITE; PS501245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bloinformat
the European Bioinformatics Institute. The
use by non-profit institutions as low
modified and this statement is not removed.
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00086; PAC;
SMART; SM00091; PAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X61458;
PIR; S31280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN-i- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003018;
InterPro; IPR003594;
                                                  382
                                                                       168
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                                                                                                                                                 263
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                                                                                                                                                                                                            KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                                                              LRYACEFLMQAFGLQLQMELQLASQLAEK
                                                                                                              GCHTQYMANMGSVASLALAIVVKGKD------
                                                LRSACEFLMQVFGLQLNMEAAVAAHVREK
                                                                                                 GCHAQYMGNMGSVASLVMAMIINDNDEPSGGGGGGGQHKGRRLWGLVVCHHTSPRSVPF-
                                                                                                                                                 EPYLGLHYPATDIPQASRFLFMKNRVRMICDCSAPPVKITQDKELRQPISLAGSTLRAPH
                                                                                                                                                              EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
                                                                                                                                                                                               KLAAKAISRLQSLPGGDIGLLCDTVVEEVRDVTGYDLVMAYKFHEDEHGEVVAEIRRSDL
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                                                                                                                                                                                                                                                                                                                                                                                             Multigene
                                                                                                                                                                                                                                                                                                           1134
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750
901
324
352
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                           ĀΑ;
                                                                                                                                                                                                                                                                                                                      family.
687
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821
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67.9%;
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HIS_KIN_sig.
                                                                                                                                                                                                                                                                                                           124706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAS-assoc_C
                                                                                                                                                                                                                                                                                                                                                                                                             Photoreceptor;
                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                           MW.
                                                                                                                                                                                                                                             Score 747; DB 1 Pred. No. 9e-68; Mismatches
                                                                                                                                                                                                                                                                                                                                                          PAS
PAC.
PAS
                                                                                                                                                                                                                                                                                                                                  HISTIDINE KINASE
CHROMOPHORE (BY
                                                                                                                                                                                                                                                                                                                        POLY-GLY
                                                                                                                                                                                                                                                                                                           42819B9F4ACC398C CRC64;
                                                                                                                                                                                                                                                                                                                                                            2
                                                                         196
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                                                                                                                       ----SSKLWGLVVGHHCSPRYVPFP
                                                                                                                                                                                                                                                                                                                                                                                                           Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                       <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                30;
                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                    Length 1134;
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Pfam; PF009b...

Pfam; PF00512; Signal,

Pfam; PF00512; Signal,

Pfam; PF00512; Signal,

Pfam; PF00512; Signal,

PRINTS; PR01033; PHYTOCHROW...

DR SMART; SM00085; GAF; 1.

DR SMART; SM00387; HATPase_C; 1.

DR SMART; SM00386; PAC; 1.

DR SMART; SM00091; PAS; 2.

PROSITE; PS50110; PAS; 2.

PROSITE; PS50112; PAS; 2.

PROSITE; PS50112; PAS; 2.

PROPER PS50112; PAS; 2.

PR
      Transcription
Repeat.
DOMAIN
DOMAIN
74
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InterPro;
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                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Physcomitrella patens (MOSS).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
NCBI_TaxID-3218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
SIMILARITY: CONTAINS 2 PAS (PER-ARMY-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
SIMILARITY: CONTAINS 1 HISTIDINE KIDASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORB MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; X75025; CAA52933.1; -. 
S37206; S37206.
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IPR001294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003594;
IPR004359;
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41,
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HIS_KIN_Sig.
His_kinA.
PAC.
31 PAS 1.

15 PAS 2.

15 HISTIDINE KINASE.

16 CHROMOPHORE (BY SIMILARITY)

125230 MW; ElDAD4D6DC9C0D16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phytochrome
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Last sequence update)
Last annotation updat
                                                                                                                                                                                      Photoreceptor; Phytochrome; Chromophore;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
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                                                                                                                                                    1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL
                                                                                                                                          KLAAKAITRLQALPGGNIGLLCDTVVEEVRELTGYDRVMAYRFHEDEHGEVVAEIRRADL
           CEFLMQAFGLQLQMELQLASQLAEK
                                                                    GCHTQYMANMGSVASLALAIVVKGKDSS------KLWGLVVGHHCSPRYVPFPLRYA
                                                                                            EPYLGLHYPGTDIPQASRFLFMKNKVRIIADCSAPPVKVIQDPTLRQPVSLAGSTLRSPH
                                                                                                                   EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH
CGFLMQVFGLQLNMEVESAAQLREK
                                              GCHAQYMGNMGSIASLVMAVIINDNEEDSHGSVQRGRKLWGLVVCHHTSPRTVPFPLRSA
                                                                                                                                                                                       136;
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66.3%;
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                                                                                                                                                                                                   Score 740.5;
Pred. No. 4.
 404
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Search completed: June 7, 2002, 18:58:04 Job time: 243 sec